



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 109990

TO: Lorraine Spector
Location: CM-1/10B11/10B19
Art Unit: 1647
Tuesday, December 09, 2003

Case Serial Number: 09/996569

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Spector,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

From: Hutzell, Paula
Sent: Monday, December 08, 2003 4:01 PM
To: Spector, Lorraine; STIC-Biotech/ChemLib
Subject: RE: 09/996569

approved

-----Original Message-----

From: Spector, Lorraine
Sent: Monday, December 08, 2003 3:53 PM
To: Hutzell, Paula
Subject: FW: 09/996569

Paula,
would you please authorize this as a rush search? Reasons evident.
Thanks,
Lori

-----Original Message-----

From: Hanley, Susan
Sent: Monday, December 08, 2003 3:51 PM
To: Spector, Lorraine
Subject: RE: 09/996569

*I'm afraid that I can't help you out with this request. As of last week, I rejoined the patent examining corps. If you want more alignments, you will have to request a new search. The standard search set-up provides 15 alignments and that's it.
The searcher cannot print out more alignments because the computer only posted 15 of the results to be displayed with alignments.
Protein searches should turn around in 2 days max.*

*Susan Hanley
US Patent and Trademark Office
Art Unit 1651
Office: 11E07 Mail Box: 11B01
Phone: 703-305-1982*

-----Original Message-----

From: Spector, Lorraine
Sent: Monday, December 08, 2003 3:41 PM
To: Hanley, Susan
Subject: 09/996569

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 12/9/03
Date Completed: 12/9/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: QSP
WWW/Internet: _____
Other (specify): _____

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpn and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapn and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

Importance: High

Susan,

You ran a search for me on this case on 11/26, on sequence ID NO:2

Could you please print out more hits for the oligo search in the .rag and .rai databases only?

I'd like to see all hits down to 10 contiguous residues.

Thanks,

Lori

Lorraine Spector, Ph.D.

Patent Examiner

U.S. Patent and Trademark Office

CM1, 10B-11

703-308-1793

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library GM1 - Circ. Desk



GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2003, 08:44:40 ; Search time 47 seconds
(without alignments)
1827.044 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGLSLHVGWMLGSL.....DILMKSPRPMSNPDTG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*
1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	100.0	541	18	AAW12695
2	363	67.1	550	22	AAW12695
3	363	67.1	550	24	ABU56732
4	363	67.1	550	24	ABP81871
5	342	63.2	561	22	ABU56731
6	262	48.4	550	22	ABU56386
7	262	48.4	550	22	AAW12695
8	38	7.0	542	22	AAW12695
9	25	4.6	515	13	AAW12695

10	25	4.6	515	17	AAW12695
11	25	4.6	515	20	AAW12695
12	25	4.6	585	13	AAW12695
13	25	4.6	585	17	AAW12695
14	25	4.6	585	22	AAW12695
15	22	4.1	864	22	AAW12695
16	20	3.7	20	24	ABP82552
17	19	3.5	440	21	AAW12695
18	19	3.5	440	22	AAW12695
19	19	3.5	440	22	AAW12695
20	19	3.5	440	23	AAW12695
21	19	3.5	440	23	AAW12695
22	19	3.5	440	24	AAW12695
23	19	3.5	449	13	AAW12695
24	18	3.3	18	24	ABP82551
25	18	3.3	324	21	AAW12695
26	18	3.3	335	21	AAW12695
27	18	3.3	435	21	AAW12695
28	18	3.3	435	21	AAW12695
29	18	3.3	446	21	AAW12695
30	18	3.3	448	21	AAW12695
31	18	3.3	450	21	AAW12695
32	18	3.3	536	21	AAW12695
33	18	3.3	536	21	AAW12695
34	18	3.3	591	13	AAW12695
35	18	3.3	591	17	AAW12695
36	18	3.3	591	20	AAW12695
37	18	3.3	593	17	AAW12695
38	18	3.3	593	20	AAW12695
39	18	3.3	593	22	AAW12695
40	18	3.3	593	22	AAW12695
41	18	3.3	593	24	ABP81872
42	18	3.3	595	24	ABG73825
43	18	3.3	614	13	AAW12695
44	16	3.0	447	23	ABW79169
45	14	2.6	19	13	AAW12695

ALIGNMENTS

RESULT 1

AAW12695
ID AAW12695 standard; Protein; 541 AA.

XX AC AAW12695;

XX AC AAW12695;

XX DT 31-MAY-1997 (first entry)

XX DT 31-MAY-1997 (first entry)

XX DE G-protein parathyroid hormone receptor HLTG74.

XX DE G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH;
KW calcium; signal transduction; agonist; antagonist; hypocalcaemia;
KW hyperphosphataemia; hypoparathyroidism; chronic tetany;
KW osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia;
KW kidney stone; nephrolisis; therapy; diagnosis.

XX OS Homo sapiens.

XX PN WO9639433-A1.

XX PN WO9639433-A1.

XX PD 12-DEC-1996.

XX PF 05-JUN-1995; 95WO-US07085.

XX PR 05-JUN-1995; 95WO-US07085.

XX PR 05-JUN-1995; 95WO-US07085.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Li Y, Rosen CA, Ruben SM, Soppet DR;

XX PI WPI; 1997-043068/04.

XX DR N-PSDB; AAT59619.

XX DR N-PSDB; AAT59619.

XX DR N-PSDB; AAT59619.

XX DR N-PSDB; AAT59619.

XX DR N-PSDB; AAT59619.

XX DR N-PSDB; AAT59619.

XX Human G-protein parathyroid hormone receptor, HLTG74 - used to
PT identify (ant)agonists, used in the treatment of hypo- or
PT hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc
XX
PS Claim 9; Fig 1A-E; 62pp; English.
XX
XX A novel 7-transmembrane receptor (AAW12695) has been identified as a
CC human G-protein parathyroid hormone (PTH) receptor, designated
CC HLTG74. It shows 48.2% homology to the human PTH receptor. Its
CC amino acid sequence was deduced from a cDNA clone (AA759619) isolated
CC from a human T cell lymphoma tissue cDNA library. Recombinant
CC HLTG74 can be produced in transformed host cells and used to
CC screen for (ant)agonist cpds. Agonists may be used to prevent or
CC treat e.g. hypocalcaemia, hyperphosphataemia, hypoparathyroidism
CC and chronic tetany by stimulating an increase in serum calcium
CC levels. Antagonists can be used to inhibit the receptor e.g. for
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,
CC hypophosphataemia, kidney stone, nephrolithiasis.
XX
SQ Sequence 541 AA;

Query Match 100.0%; Score 541; DB 18; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLASLHWGMLGSCLLARAQLDSGTITIEQIVLVKAKVQCELNITAOQEGR 60
Db 1 MAWLGLASLHWGMLGSCLLARAQLDSGTITIEQIVLVKAKVQCELNITAOQEGR 60

QY 61 GNCFFPMDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
Db 61 GNCFFPMDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTTWA 120

QY 121 NYSDCFLRFLQPDISIGKQEFCEFLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
Db 121 NYSDCFLRFLQPDISIGKQEFCEFLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180

QY 181 MHLFVSMFLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDKSQYIGCKIAV 240
Db 181 MHLFVSMFLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDKSQYIGCKIAV 240

QY 241 VMFIYLATNYWILVEGLYHLNLI FVAFPSDTKYLWGFTLLIGWGFPAFVAWAVARAT 300
Db 241 VMFIYLATNYWILVEGLYHLNLI FVAFPSDTKYLWGFTLLIGWGFPAFVAWAVARAT 300

QY 301 LADARCWELSAGDIKWIYQAPILAAAGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSAGDIKWIYQAPILAAAGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360

QY 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWETRMHCELPFNSFQGFVSIYCYCNGEV 420
Db 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWETRMHCELPFNSFQGFVSIYCYCNGEV 420

QY 421 QAEVKKWRNLSVDWKRTPPCGSRRCGSVLTVTHSTSSQQAHAHAWCLSLAKLPR 480
Db 421 QAEVKKWRNLSVDWKRTPPCGSRRCGSVLTVTHSTSSQQAHAHAWCLSLAKLPR 480

QY 481 SPADSLTATSLYLAAGVTSQRTASHTLSTRNKEDSGQRDDILMEKPSRPMSNPDT 540
Db 481 SPADSLTATSLYLAAGVTSQRTASHTLSTRNKEDSGQRDDILMEKPSRPMSNPDT 540

QY 541 G 541
Db 541 G 541

RESULT 2

AAB71875

ID AAB71875 standard; Protein: 550 AA.

XX

AC AAB71875;

XX

DT 03-MAY-2001 (first entry)
XX
DE Human PTH2 seven transmembrane domain.
XX
KW Human; PTH2; parathyroid hormone receptor; h15571; immunomodulatory;
KW vascular; hepatic; antiasthma; antimicrobial; antiinflammatory;
KW immunosuppressive; gene therapy; vaccine; G-protein coupled receptor;
KW GPCR; liver fibrosis; respiratory disorder; infection;
KW chronic inflammatory disease; organ-specific autoimmunity;
KW graft rejection; cystic fibrosis.
XX
OS Homo sapiens.
XX
PN WO200109328-A1.
XX
PD 08-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-US21278.
XX
PR 03-AUG-1999; 99US-0146916.
PR 29-FEB-2000; 2000US-0515781.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA Hodge MR, Lloyd C, Weich NS;
XX
PI WPI; 2001-138653/14.
XX
DR Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
PT -
XX
XX Disclosure; Fig 2; 145pp; English.
XX
CC The present sequence is a human G-protein coupled receptor (GPCR) used
CC for comparison with the seven transmembrane domain of a novel GPCR
CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate GPCR expression. Such diseases includes immune,
CC haematological, fibrotic, hepatic and respiratory disorders including
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
CC graft rejection, graft versus host disease, cystic fibrosis and, in
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
CC in the production of antibodies against GPCR and in assays to identify
CC modulators (agonists and antagonists) of GPCR expression and activity.
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
CC used as diagnostic agents for detecting the presence of GPCR
CC polypeptides in samples.
XX
SQ Sequence 550 AA;

Query Match 67.1%; Score 363; DB 22; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LCASLHWGMLGSCLLARAQLDSGTITIEQIVLVKAKVQCELNITAOQEGRNC 63
Db 4 LCASLHWGMLGSCLLARAQLDSGTITIEQIVLVKAKVQCELNITAOQEGRNC 63

QY 64 FPEWDLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTTWANTS 123
Db 64 FPEWDLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTTWANTS 123

QY 124 DCLRFLOPDISIGKQEFCEFLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTHMEL 183
Db 124 DCLRFLOPDISIGKQEFCEFLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTHMEL 183

QY 184 FVSMFLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDKSQYIGCKIAVNF 243
Db 184 FVSMFLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDKSQYIGCKIAVNF 243

QY 244 IYFLATNYWILVEGLYLHNLIFVAFSDTKYLWGLFILLGMPFAAFVAAWAVARATLAD 303
Db 244 IYFLATNYWILVEGLYLHNLIFVAFSDTKYLWGLFILLGMPFAAFVAAWAVARATLAD 303
QY 304 ARCWELSGDIIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDTKQYRKLAK 363
Db 304 ARCWELSGDIIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDTKQYRKLAK 363
QY 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRHMCLELFPNSFGQFFVSIYCYCNGEVOAE 423
Db 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRHMCLELFPNSFGQFFVSIYCYCNGEVOAE 423
QY 424 VKQWRSRWNLSDVWKRTPPCGSRRCGSLTITVTHSTSSQSOVAA 467
Db 424 VKQWRSRWNLSDVWKRTPPCGSRRCGSLTITVTHSTSSQSOVAA 467

RESULT 3

ABU56732
ID ABU56732 standard; Protein; 550 AA.
AC ABU56732;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #325.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiaesthetic; non-small cell lung cancer;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
FN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US2476.
XX
PR 18-APR-2001; 2001US-284770P.
PR 10-MAY-2001; 2001US-290492P.
PR 09-NOV-2001; 2001US-339245P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-NOV-2001; 2001US-334370P.
PR 12-APR-2002; 2002US-372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI; 2003-093161/08.
DR N-PSDB; ABX76461.
XX

PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer -
XX
XX Claim 27; Page 439-440; 453pp; English.
PS
XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung

CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
CC polypeptides of the invention.
XX
SQ Sequence 550 AA;
Query Match 67.1%; Score 363; DB 24; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 LGASLHVWGLMGLSCLLARAQLSDGTITIEEQILVLKAKVQCELNITLAQLQEGGNC 63
Db 4 LGASLHVWGLMGLSCLLARAQLSDGTITIEEQILVLKAKVQCELNITLAQLQEGGNC 63
QY 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCPNPGTDFMHSINKTWANYS 123
Db 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCPNPGTDFMHSINKTWANYS 123
QY 124 DCLRFLOPDISIGKQEFCEERLYVMYTVGYSISFGSLAVAILIIGYFRHLHCTRYIHWHL 183
Db 124 DCLRFLOPDISIGKQEFCEERLYVMYTVGYSISFGSLAVAILIIGYFRHLHCTRYIHWHL 183
QY 184 FVSPMLRATSFVDRVVRVHAHIGVKELESIMQDDPQNSIEATSVDSQYIGCKIAVWVF 243
Db 184 FVSPMLRATSFVDRVVRVHAHIGVKELESIMQDDPQNSIEATSVDSQYIGCKIAVWVF 243
QY 244 IYFLATNYWILVEGLYLHNLIFVAFSDTKYLWGLFILLGMPFAAFVAAWAVARATLAD 303
Db 244 IYFLATNYWILVEGLYLHNLIFVAFSDTKYLWGLFILLGMPFAAFVAAWAVARATLAD 303
QY 304 ARCWELSGDIIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDTKQYRKLAK 363
Db 304 ARCWELSGDIIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDTKQYRKLAK 363
QY 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRHMCLELFPNSFGQFFVSIYCYCNGEVOAE 423
Db 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRHMCLELFPNSFGQFFVSIYCYCNGEVOAE 423
QY 424 VKQWRSRWNLSDVWKRTPPCGSRRCGSLTITVTHSTSSQSOVAA 467
Db 424 VKQWRSRWNLSDVWKRTPPCGSRRCGSLTITVTHSTSSQSOVAA 467

RESULT 4

ABP81871
ID ABP81871 standard; Protein; 550 AA.
XX
AC ABP81871;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human parathyroid hormone receptor 2 protein SEQ ID NO:227.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX
XX Homo sapiens.
XX
XX WO200261087-A2.
FN

XX PD 08-AUG-2002.

XX PF 19-DEC-2001; 2001WO-US50107.

XX PR 19-DEC-2000; 2000US-257144P.

XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burner GC, Roush CL, Brown JP;

XX DR WPI; 2003-046718/04.

XX DR N-PSDB; AB242718.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors

PT (GPCR), useful for diagnosing and designing drugs for treating

PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,

PT cancer or autoimmune diseases -

XX

PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising:

CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino

CC acids. Also described: (1) an assay for the detection of a particular

CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;

CC and (2) an isolated antibody having high specificity and high affinity

CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and

CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting

CC an antibody against a particular GPCR, and in the production of specific

CC antibodies. The peptides and antibodies are also useful for detecting the

CC presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for

CC treating immune-related diseases, growth-related diseases, cell

CC regeneration-related disease, immunological-related diseases, cell

CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,

CC atherosclerosis, bacterial, fungal, protozoan or viral infections,

CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute

CC inflammation, allergies, Crohn's disease, diabetes, graft versus host

CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,

CC anxiety, depression, schizophrenia, dementia, mental retardation, memory

CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,

CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or

CC any other disorder in which GPCRs are involved. The antibodies may be

CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode

CC GPCR proteins given in ABP81675 to ABP82018, which are used in the

CC exemplification of the present invention.

XX

SQ Sequence 550 AA;

Query Match 67.1%; Score 363; DB 24; Length 550;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LGASHVWGMVLMGSLARALQSDGTTTIEQIVLVKAKVQCELNITAIQIQEGNC 63

DB 4 LGASHVWGMVLMGSLARALQSDGTTTIEQIVLVKAKVQCELNITAIQIQEGNC 63

QY 64 FPEWDLICWPRTGTVGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKWTWYNS 123

DB 64 FPEWDLICWPRTGTVGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKWTWYNS 123

QY 124 DCLRFLOPDISIGKQFCRRLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNHML 183

DB 124 DCLRFLOPDISIGKQFCRRLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNHML 183

QY 184 FVSEMLRATSIYKORVVAHHTGVKELESILNQDDPQNSIATSVKQYIGCKIAVVMF 243

DB 184 FVSEMLRATSIYKORVVAHHTGVKELESILNQDDPQNSIATSVKQYIGCKIAVVMF 243

QY 244 IYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAFVAWAARATLAD 303

DB 244 IYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAFVAWAARATLAD 303

QY 304 ARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRKLAK 363

DB 304 ARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRKLAK 363

QY 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFFVSIYCYCNGEVQAE 423

DB 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFFVSIYCYCNGEVQAE 423

QY 424 VKKMSRWNLSDVWKRTPPCGSRRRCGSLVTTVTHSTSSQSVAA 467

DB 424 VKKMSRWNLSDVWKRTPPCGSRRRCGSLVTTVTHSTSSQSVAA 467

RESULT 5

ABU56731

ID ABU56731 standard; Protein; 561 AA.

XX AC ABU56731;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polypeptide #324.

XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;

XX KW antinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;

XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.

XX PN WO200286443-A2.

XX PD 31-OCT-2002.

XX PF 18-APR-2002; 2002WO-US12476.

XX PR 18-APR-2001; 2001US-284770P.

XX PR 10-MAY-2001; 2001US-290492P.

XX PR 09-NOV-2001; 2001US-339245P.

XX PR 13-NOV-2001; 2001US-350666P.

XX PR 29-NOV-2001; 2001US-334370P.

XX PR 12-APR-2002; 2002US-372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Aziz N, Murray R;

XX DR WPI; 2003-093161/08.

XX N-PSDB; ABX76460.

PT Detecting a lung cancer-associated transcript in a cell from a patient

PT for treating lung cancer, by contacting a biological sample from the

PT patient with a polynucleotide that exhibits increased or decreased

PT expression in lung cancer -

XX

PS Claim 27; Page 439; 453pp; English.

XX

CC The invention relates to a method for detecting a lung cancer-associated

CC transcript in a cell from a patient, comprising contacting a biological

CC sample from the patient with a polynucleotide that selectively hybridizes

CC to a sequence that is at least 80 % identical to a gene that exhibits

CC increased or decreased expression in lung cancer samples. Lung

CC cancer-associated polynucleotides and polypeptides are used for

CC identifying a compound that modulates a lung cancer-associated

CC polypeptide, for inhibiting proliferation of a lung cancer-associated

CC cell to treat lung cancer in a patient and for treating a mammal having

CC lung cancer by administering a modulatory compound identified. The

CC methods are useful for treating lung cancer, such as small cell lung

CC cancer, non-small cell lung cancer or other benign or precancerous

CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive

CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial

CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides

CC and polypeptides are useful for diagnostic purposes and as targets for
 CC screening for therapeutic compounds that modulate lung cancer, such as
 CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
 CC polypeptides of the invention.

XX SQ Sequence 561 AA;

Query Match 63.2%; Score 342; DB 24; Length 561;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 QLDSDGTITIEQIVLVKAKVQCEINITAIQOEGEGNCFPPWDGLICWPRGTGKISAV 84
 DB 36 QLDSDGTITIEQIVLVKAKVQCEINITAIQOEGEGNCFPPWDGLICWPRGTGKISAV 95

QY 85 PCPPYIDFNHKGVAFRHCPNPGTDFMHSLNKTWANSYDCLRFLOPDISIGKQEFRR 144
 DB 96 PCPPYIDFNHKGVAFRHCPNPGTDFMHSLNKTWANSYDCLRFLOPDISIGKQEFRR 155

QY 145 YMYTVGYSISFGSLAVAILIIGYFRRLHCTRNHYHMLFVSPMLRATSIKVRVVAH 204
 DB 156 YMYTVGYSISFGSLAVAILIIGYFRRLHCTRNHYHMLFVSPMLRATSIKVRVVAH 215

QY 205 IGKLESLIMODDPQNSIEATSVKSOYIGCKIAVVMFIYFLATNYWILVEGLYHNL 264
 DB 216 IGKLESLIMODDPQNSIEATSVKSOYIGCKIAVVMFIYFLATNYWILVEGLYHNL 275

QY 265 IFVAFSDTKYLMGFLILGWGFPAAFAVAWAVARATLADARCWELSGDIKIYQAPILA 324
 DB 276 IFVAFSDTKYLMGFLILGWGFPAAFAVAWAVARATLADARCWELSGDIKIYQAPILA 335

QY 325 AIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLAKSTVLVLVFGVHHIVFVCLPH 384
 DB 336 AIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLAKSTVLVLVFGVHHIVFVCLPH 395

QY 385 SFTGLGWEIRMHCELPNSFQGFVSIYCYCNGEVOAEVKKWWSRWNLSDWKRTPPCG 444
 DB 396 SFTGLGWEIRMHCELPNSFQGFVSIYCYCNGEVOAEVKKWWSRWNLSDWKRTPPCG 455

QY 445 SRRCGSVLTVTHSTSSQSVAA 467
 DB 456 SRRCGSVLTVTHSTSSQSVAA 478

RESULT 6
 ABB56386
 ID ABB56386 standard; Protein; 550 AA.

AC ABB56386;

XX 18-FEB-2002 (first entry)

DE Non-endogenous human GPCR protein, SEQ ID NO: 565.

XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 XX constitutively activated GPCR; agonist; disease.

OS Homo sapiens.
 OS Synthetic.

XX WO200177172-A2.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-US11098.

XX 07-APR-2000; 2000US-195747P.

XX (AREN-) ARENA PHARM INC.

XX Lehmann-Bruinsma K, Liaw CW, Lin I;

XX WPI; 2001-648759/74.

DR N-PSDB; AB198022.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with
 PT versions of GPCRs -

XX Claim 1; Page 367-369; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous
 CC constitutively activated versions of known GPCRs are used in the
 CC invention for the direct identification of candidate compounds as
 CC receptor agonists, inverse agonists or partial agonists. Such
 CC agonists are useful as therapeutic agents for diseases or disorders
 CC associated with GPCRs. The present sequence is a non-endogenous
 CC version of a known human GPCR.

XX SQ Sequence 550 AA;

Query Match 48.4%; Score 262; DB 22; Length 550;
 Best Local Similarity 99.6%; Pred. No. 2.1e-259;
 Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LGASLHVGMWMLGSCLLARAQQLDSGTITIEQIVLVKAKVQCEINITAIQOEGEGNC 63

DB 4 LGASLHVGMWMLGSCLLARAQQLDSGTITIEQIVLVKAKVQCEINITAIQOEGEGNC 63

QY 64 FPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPGTDFMHSLNKTWANS 123

DB 64 FPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPGTDFMHSLNKTWANS 123

QY 124 DCLRFLOPDISIGKQEFRRLYMYTVGYSISFGSLAVAILIIGYFRRLHCTRNHYHML 183

DB 124 DCLRFLOPDISIGKQEFRRLYMYTVGYSISFGSLAVAILIIGYFRRLHCTRNHYHML 183

QY 184 FVSPMLRATSIKVRVVAHIGVKELESIMODDPQNSIEATSVKSOYIGCKIAVVMF 243

DB 184 FVSPMLRATSIKVRVVAHIGVKELESIMODDPQNSIEATSVKSOYIGCKIAVVMF 243

QY 244 IYFLATNYWILVEGLYHNLIFVAFSDTKYLMGFLILGWGFPAAFAVAWAVARATLAD 303

DB 244 IYFLATNYWILVEGLYHNLIFVAFSDTKYLMGFLILGWGFPAAFAVAWAVARATLAD 303

QY 304 ARCWELSGADIKIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLAK 363

DB 304 ARCWELSGADIKIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLAK 363

QY 364 STLVLVLVFGVHHIVFVCLPHSFTGLGWEIRMHCELPNSFQGFVSIYCYCNGEVOAE 423

DB 364 SPLVLVLVFGVHHIVFVCLPHSFTGLGWEIRMHCELPNSFQGFVSIYCYCNGEVOAE 423

QY 424 VKKWSRWNLSDWKRTPPCGSRRRCGSLTVTHSTSSQSVAA 467

DB 424 VKKWSRWNLSDWKRTPPCGSRRRCGSLTVTHSTSSQSVAA 467

RESULT 7

AAB80560

ID AAB80560 standard; Protein; 550 AA.

XX AAB80560;

XX 26-APR-2001 (first entry)

XX Human PTH2 receptor amino acid sequence.

XX Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiac;
 KW cyostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;

KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 XX leukodystrophy.
 OS Homo sapiens.
 XX WO200077042-A2.
 PN 21-DEC-2000.
 XX 15-JUN-2000; 2000WO-US16776.
 XX 15-JUN-1999; 99US-0139335.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Usdin TB, Hoare SRJ;
 XX WPI; 2001-122833/13.
 XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX Example 4; Fig I; 106pp; English.
 XX The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC anxiolytic, analgesic, antiasthmatic, antidiabetic, osteoprotective,
 CC hypertensive, cardiastatic, cytotonic, antidiabetic, osteoprotective,
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. The present
 CC sequence represents a PTH2 receptor which is used in the
 XX exemplification of the present invention.
 XX Sequence 550 AA;
 Query Match 48.4%; Score 262; DB 22; Length 550;
 Best Local Similarity 99.6%; Pred. No. 2.1e-259;
 Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 LGASLHVWGMMLGSCLLARAQLDSGTITIEEQIVLVKAKVQCELNITAIQIQEGNC 63
 DB 4 LGASLHVWGMMLGSCLLARAQLDSGTITIEEQIVLVKAKVQCELNITAIQIQEGNC 63
 QY 64 FPEWGLICWPRGTGKISAVCPPIYDFNKHGVAFRNCNPNGTWDFMHSINKTWANYS 123
 DB 64 FPEWGLICWPRGTGKISAVCPPIYDFNKHGVAFRNCNPNGTWDFMHSINKTWANYS 123
 QY 124 DCLRFLOPDISIGKQFCELYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNHML 183
 DB 124 DCLRFLOPDISIGKQFCELYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNHML 183
 QY 184 FVSFMLRATSIKVRDVAHIGVKELESIMODDPQNSIATSVDSKQYIGCKIAVVMF 243
 DB 184 FVSFMLRATSIKVRDVAHIGVKELESIMODDPQNSIATSVDSKQYIGCKIAVVMF 243
 QY 244 IYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAFVAAMAVARATLAD 303
 DB 244 IYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAFVAAMAVARATLAD 303
 QY 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLAK 363

DB 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLAK 363
 QY 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEVQAE 423
 DB 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEVQAE 423
 QY 424 VKQMSRWNLSDVMKRTPPCGSRRCGSLTVTTHSTSSQSQVAA 467
 DB 424 VKQMSRWNLSDVMKRTPPCGSRRCGSLTVTTHSTSSQSQVAA 467
 RESULT 8
 AAB80559
 ID AAB80559 standard; Protein; 546 AA.
 XX
 AC AAB80559;
 XX
 DT 26-APR-2001 (first entry)
 XX
 DE Rat PTH2 receptor amino acid sequence.
 XX
 KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; neuroleptic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antiasthmatic; antidiabetic; osteoprotective; hypertensive; cardiastatic;
 KW cytotonic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX Rattus sp.
 XX WO200077042-A2.
 XX 21-DEC-2000.
 XX 15-JUN-2000; 2000WO-US16776.
 XX 15-JUN-1999; 99US-0139335.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Usdin TB, Hoare SRJ;
 XX WPI; 2001-122833/13.
 XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX Example 4; Fig I; 106pp; English.
 XX The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC anxiolytic, analgesic, antiasthmatic, antidiabetic, osteoprotective,
 CC hypertensive, cardiastatic, cytotonic, antidiabetic, osteoprotective,
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. The present
 CC sequence represents a PTH2 receptor which is used in the
 XX exemplification of the present invention.

DT 08-FEB-1999 (first entry)

XX DE Parathyroid hormone receptor OK-H.
 XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
 KW KW PTH-related hypercalcaemia; opossum.
 XX OS Didelphis virginiana.
 XX PN US5840853-A.
 XX PD 24-NOV-1998.
 XX XX
 XX PF 06-JUN-1995; 95US-0471494.
 XX PR 06-APR-1992; 92US-0864475.
 XX PR 05-APR-1991; 91US-0681702.
 XX PR 06-JUN-1995; 95US-0471494.
 XX PA (GEOH) GEN HOSPITAL CORP.
 XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI PI Schipani E, Segre GV;
 XX DR WPI; 1999-034124/03.
 XX DR N-PSDB; AAV08388.
 XX PT Antibody to parathyroid hormone receptor - for diagnostic or
 PT PT therapeutic use
 XX PS Claim 6; Fig 1; 63pp; English.
 XX CC This sequence represents the opossum parathyroid hormone (PTH) receptor
 CC CC OK-H, which is targeted by the antibody of the invention. The antibody
 CC CC of the invention is immunoreactive with naturally occurring human, rat or
 CC CC opossum PTH receptor. The antibody is useful for treating disorders
 CC CC characterised by overstimulation of PTH receptors by their ligand and for
 CC CC the diagnosis of PTH-related hypercalcaemia.
 XX SQ Sequence 515 AA;
 Query Match 4.6%; Score 25; DB 20; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1.7e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRRLHCTRNTHMHLFVSFMLRA 191
 Db 207 GYFRRLHCTRNTHMHLFVSFMLRA 231
 RESULT 12
 AAR27705
 ID AAR27705 standard; Protein; 585 AA.
 XX AC AAR27705;
 XX DT 25-MAR-2003 (updated)
 XX DT 16-MAR-1993 (first entry)
 XX DE Opossum kidney PTH/PTHrP receptor prod. from clone OK-O.
 XX DE Parathyroid hormone; related protein; calcium; antagonist;
 KW KW antibodies; hypercalcaemia.
 XX OS Didelphis virginiana.
 XX PN WO9217602-A1.
 XX PD 15-OCT-1992.
 XX PF 06-APR-1992; 92WO-US02821.
 XX PR 05-APR-1991; 91US-0681702.
 XX PR 06-APR-1992; 92US-0864475.

XX PA (GEOH) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
 XX PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
 PI PI Segre GV;
 XX DR WPI; 1992-366271/44.
 XX DR N-PSDB; AAQ29605.
 XX PT New DNA encoding parathyroid hormone receptor, DNA and antibodies
 PT PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
 PT PT and treatment of tumours
 XX PS Disclosure; Fig 2; 91pp; English.
 XX CC The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
 CC CC receptor protein sequence was deduced from the DNA sequence of the
 CC CC clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O
 CC CC is identical to the OK-H clone except at the C-terminal tail as OK-O
 CC CC encodes a 595 amino acid protein, OK-H encodes one of 515 amino acids.
 CC CC The difference is attributed to a single nucleotide deleted in the OK-H
 CC CC sequence causing a frame shift and an earlier stop codon. It is not
 CC CC known whether OK-O and OK-H represent prods. of two separate genes or
 CC CC are a laboratory artifact. The protein may be used in a therapeutic
 CC CC compen. to inhibit activation of PTH or PTHrP and thus reduce the
 CC CC level of calcium in the blood. Cpd. capable of competing with PTH
 CC CC or PTHrP for binding can be identified using the protein prod. and
 CC CC DNAs homologous to PTH DNA can be identified using fragments of the
 CC CC clone as probes. The sequence may be used for the prod. of antibodies
 CC CC useful for the treatment, classification, prognosis and/or treatment of
 CC CC disorders related to the interaction between a cell receptor and a
 CC CC ligand such as in hypercalcaemia. See also AAR27704-16.
 CC CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 585 AA;
 Query Match 4.6%; Score 25; DB 13; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.9e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRRLHCTRNTHMHLFVSFMLRA 191
 Db 207 GYFRRLHCTRNTHMHLFVSFMLRA 231
 RESULT 13
 AAR92276
 ID AAR92276 standard; Protein; 585 AA.
 XX AC AAR92276;
 XX DT 25-MAR-2003 (updated)
 XX DT 18-MAY-1996 (first entry)
 XX DE Opossum kidney PTH/PTHrP receptor.
 XX DE Parathyroid hormone; receptor; parathormone; PTH;
 KW KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
 KW KW hypercalcaemia; hypocalcaemia; cancer; opossum.
 XX OS Didelphis virginiana.
 XX PN US5494806-A.
 XX PD 27-FEB-1996.
 XX PF 06-APR-1992; 92US-0864475.
 XX PR 06-APR-1992; 92US-0864475.
 XX PR 05-APR-1991; 91US-0681702.
 XX PA (GEOH) GEN HOSPITAL CORP.
 XX XX

PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX WPI; 1996-139028/14.
 DR N-PSDB; AAT15946.
 CC
 PT DNA encoding vertebrate parathyroid hormone receptor - useful for
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
 PT cancer etc.
 XX
 PS Claim 1; Fig 2A-2E; 64pp; English.
 XX
 CC Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
 CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
 CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
 CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
 CC separate genes or of a laboratory artifact. The receptor induces an
 CC increase in intracellular cAMP and calcium when challenged with PTH or
 CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
 CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
 CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
 CC Host cells expressing the receptor can be used for diagnostic
 CC measurement of PTH serum levels.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 585 AA;
 Query Match 4.6%; Score 25; DB 17; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.9e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRLHCTRYIHMLFVSFMLRA 191
 Db 207 GYFRLHCTRYIHMLFVSFMLRA 231
 RESULT 14
 AAW73315
 ID AAW73315 standard; Protein; 585 AA.
 AC AAW73315;
 DT 08-FEB-1999 (first entry)
 XX Parathyroid hormone receptor OK-O.
 XX Parathyroid hormone receptor; PTH receptor; antibody; therapy;
 KW PTH-related hypercalcaemia; opossum.
 XX Didelphis virginiana.
 XX US5840853-A.
 PN 24-NOV-1998.
 XX 06-JUN-1995; 95US-0471494.
 XX 06-APR-1992; 92US-0864475.
 PR 05-APR-1991; 91US-0681702.
 PR 06-JUN-1995; 95US-0471494.
 XX (GEO) GEN HOSPITAL CORP.
 XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX WPI; 1999-034124/03.
 DR N-PSDB; AAV08389.
 XX Antibody to parathyroid hormone receptor - for diagnostic or
 PT therapeutic use
 XX
 PS Claim 6; Fig 2; 63pp; English.

XX This sequence represents the opossum parathyroid hormone (PTH) receptor
 CC OK-O, which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat or
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.
 XX
 SQ Sequence 585 AA;
 Query Match 4.6%; Score 25; DB 20; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.9e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRLHCTRYIHMLFVSFMLRA 191
 Db 207 GYFRLHCTRYIHMLFVSFMLRA 231
 RESULT 15
 ABG27219
 ID ABG27219 standard; Protein; 864 AA.
 AC ABG27219;
 XX 18-FEB-2002 (first entry)
 DT Novel human diagnostic protein #27210.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX Food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US08631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 DR N-PSDB; AAS91406.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 20; SEQ ID No 57578; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 864 AA;

Query Match 4.1%; Score 22; DB 22; Length 864;
 Best Local Similarity 100.0%; Pred. No. 3.2e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LGASLHVGMMLGSCLLARAQ 25
 DB 4 LGASLHVGMMLGSCLLARAQ 25

RESULT 16
 ABP82552
 ID ABP82552 standard; Peptide; 20 AA.
 XX AC ABP82552;
 XX DT 04-MAR-2003 (first entry)
 XX DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1225.
 XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

OS Homo sapiens.
 XX WO200261087-A2.
 XX 08-AUG-2002.
 XX 19-DEC-2001; 2001WO-US50107.
 XX 19-DEC-2000; 2000US-257144P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX Burmer GC, Roush CL, Brown JP;
 XX WPI; 2003-046718/04.
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -
 XX Claim 1; Fig 2; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for

CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnoses. ABP82552 to ABP82869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 20 AA;

Query Match 3.7%; Score 20; DB 24; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 ESLIMODDPONSIEATSVDK 230
 DB 1 ESLIMODDPONSIEATSVDK 20

RESULT 17
 AAB08188
 ID AAB08188 standard; Protein; 440 AA.
 XX AC AAB08188;
 XX DT 04-DEC-2000 (first entry)
 XX DE Amino acid sequence of rat secretin receptor polypeptide.
 KW Secretin; gastrointestinal hormone; pancreatic fluid; S cell;
 KW pancreatic cell growth; pancreatic beta cell; pancreatic islet;
 KW insulin production; glucose metabolism; insulin resistance;
 KW glucose intolerance; hyperglycemia; hyperinsulinemia; obesity;
 KW hyperlipidemia; hyperproteinemia; Type II diabetes mellitus;
 KW secretin receptor.

XX Rattus sp.
 XX WO200047721-A2.
 XX 17-AUG-2000.
 XX 10-FEB-2000; 2000WO-US03422.
 XX 10-FEB-1999; 99US-0119575.
 XX (ONTO-) ONTOGENY INC.
 XX Kagan D, Pang K;
 XX WPI; 2000-515058/46.
 XX N-PSDB; AAA63813.

XX Secretin therapeutic is used to modulate the growth state of pancreatic
 PT cells to provide treatment for diabetes through modification of glucose
 PT metabolism -

XX Disclosure; Page 88-90; 90pp; English.

XX The present sequence represents a rat secretin receptor polypeptide.
 CC Secretin is a gastrointestinal hormone that stimulates the secretion of
 CC bicarbonate-rich pancreatic fluid. Secretin is produced by specific
 CC endocrine cells (S cells) located in the mucosa of the proximal small
 CC intestine. Secretion of secretin is stimulated by the presence of either
 CC acidic pH or fatty acids in the duodenum. The specification describes
 CC a method for modulating the growth state of pancreatic cells. The method

CC comprises contacting the cells with a secretin therapeutic or prodru
 CC form of secretin. Secretin is used to modulate the growth state of
 CC pancreatic cells, in particular to promote the proliferation of
 CC pancreatic cells, generate functional pancreatic beta cells from
 CC pancreatic islets or cells, promote insulin production in a pancreatic
 CC islet or cell, antagonize insulin inhibition of secretin response in
 CC secretin-responsive cells, modify glucose metabolism in an animal to
 CC treat a disease associated with altered glucose metabolism e.g. insulin
 CC resistance, glucose intolerance or non-responsiveness, hyperglycemia,
 CC hyperinsulinemia, obesity, hyperlipidemia, hyperproteinemia or Type II
 CC diabetes mellitus (NIDDM).
 XX
 SQ Sequence 440 AA;

Query Match 3.5%; Score 19; DB 21; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIHMLFVSF 187
 |||||
 Db 167 FRLHCTRNVIHMLFVSF 185

RESULT 18
 ABB56387
 ID ABB56387 standard; Protein; 440 AA.
 XX
 AC ABB56387;

DT 18-FEB-2002 (first entry)

DE Non-endogenous human GPCR protein, SEQ ID NO: 567.

XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 KW constitutively activated GPCR; agonist; disease.
 XX
 OS Homo sapiens.
 OS Synthetic.

PN WO200177172-A2.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-US11098.

XX 07-APR-2000; 2000US-195747P.

XX (AREN-) ARENA PHARM INC.

XX Lehmann-Bruinsma K, Liaw CW, Lin I;

XX WPI; 2001-648759/74.

DR N-PSDB; ABI98023.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with
 PT versions of GPCRs -

XX Claim 1; Page 370-371; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous
 CC constitutively activated versions of known GPCRs are used in the
 CC invention for the direct identification of candidate compounds as
 CC receptor agonists, inverse agonists or partial agonists. Such
 CC agonists are useful as therapeutic agents for diseases or disorders
 CC associated with GPCRs. The present sequence is a non-endogenous
 CC version of a known human GPCR.

SQ Sequence 440 AA;

Query Match 3.5%; Score 19; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIHMLFVSF 187
 |||||
 Db 167 FRLHCTRNVIHMLFVSF 185

RESULT 19
 AAB71877
 ID AAB71877 standard; Protein; 440 AA.
 XX
 AC AAB71877;

DT 03-MAY-2001 (first entry)

DE Human SCRC seven transmembrane domain.

XX Human; SCRC; secretin receptor; h15571; immunomodulatory; vascular;
 KW hepatic; antiasthma; antimicrobial; antiinflammatory; immunosuppressive;
 KW gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis;
 KW respiratory disorder; infection; chronic inflammatory disease;
 KW organ-specific autoimmunity; graft rejection; cystic fibrosis.

XX Homo sapiens.

XX WO200109328-A1.

XX 08-FEB-2001.

XX 03-AUG-2000; 2000WO-US21278.

XX 03-AUG-1999; 99US-0146916.

PR 29-FEB-2000; 2000US-0515781.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hodge MR, Lloyd C, Weich NS;

XX WPI; 2001-138653/14.

XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma

XX Disclosure; Fig 2; 145pp; English.

XX The present sequence is a human G-protein coupled receptor (GPCR) used
 CC for comparison with the seven transmembrane domain of a novel GPCR
 CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate GPCR expression. Such diseases include immune,
 CC haematological, fibrotic, hepatic and respiratory disorders including
 CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
 CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
 CC graft rejection, graft versus host disease, cystic fibrosis and, in
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
 CC in the production of antibodies against GPCR and in assays to identify
 CC modulators (agonists and antagonists) of GPCR expression and activity.
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
 CC used as diagnostic agents for detecting the presence of GPCR
 CC polypeptides in samples.

SQ Sequence 440 AA;

Query Match 3.5%; Score 19; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIHMLFVSF 187
 |||||
 Db 167 FRLHCTRNVIHMLFVSF 185

RESULT 20
 ABB08012
 ID ABB08012 standard; Protein; 440 AA.
 AC ABB08012;
 DT 27-AUG-2002 (first entry)
 XX
 DE Protein identified by trembl Accession No. AB109120.
 XX
 KW Secretin receptor-like GPCR; G-protein coupled receptor; GPCR; human;
 KW uropathic; cytosolic; antischizophrenic; tranquilizer; antidepressant;
 KW hypotensive; antimigraine; anorectic; nootropic; neuroprotective;
 KW antiemetic.
 XX
 OS Homo sapiens.
 PN WO200229050-A2.
 PD 11-APR-2002.
 PF 04-OCT-2001; 2001WO-EP11442.
 PR 06-OCT-2000; 2000US-238045P.
 XX 31-AUG-2001; 2001US-315958P.
 PA (FARB) BAYER AG.
 PI Liou J;
 PS WPI; 2002-362601/39.
 XX
 PT An isolated polynucleotide encoding a secretin receptor-like G-protein
 PT coupled receptor polypeptide, for identifying reagents which modulate
 PT its function used to treat e.g. obesity, cancer and diabetes -
 XX
 PS Disclosure; Fig 3; 133pp; English.
 XX
 CC The invention relates to a human secretin receptor-like G-protein coupled
 CC receptor (GPCR) polypeptide and encoding polynucleotide. An expression
 CC vector comprising the polynucleotide is useful for preparing a medicament
 CC for modulating the activity of a secretin receptor-like GPCR in a disease
 CC such as urinary incontinence, benign prostate hyperplasia, obesity,
 CC cancer, diabetes, osteoporosis, anxiety, depression, hypertension,
 CC migraine, compulsive disorder, schizophrenia, autism, a neurodegenerative
 CC disorder, or cancer chemotherapy-induced vomiting. These diseases may
 CC also be treated by reagents which modulate a function of a human secretin
 CC receptor like GPCR, where symptoms of the secretin receptor-like GPCR
 CC dysfunction are ameliorated. The present sequence represents a protein
 CC identified by trembl Accession No. AB109120.
 XX
 SQ Sequence 440 AA;
 Query Match 3.5%; Score 19; DB 23; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 169 FRLHCTRNTHMHLFVSP 187
 Db 167 FRLHCTRNTHMHLFVSP 185
 RESULT 21
 ABB81202
 ID ABB81202 standard; Protein; 440 AA.
 AC ABB81202;
 DT 13-AUG-2002 (first entry)
 XX
 DE Human secretin receptor-like GPCR related protein SEQ ID NO:3.
 XX

KW Human; secretin; secretin receptor-like G protein-coupled receptor;
 KW secretin receptor-like GPCR; receptor; uropathic; cytosolic; anorectic;
 KW antidiabetic; osteopathic; tranquilizer; antidepressant; hypotensive;
 KW antimigraine; neuroleptic; nootropic; antiemetic; gene therapy; vaccine;
 KW antisense therapy; protein therapy; urinary incontinence, obesity;
 KW benign prostate hyperplasia; cancer; diabetes; osteoporosis; anxiety;
 KW depression; hypertension; migraine; compulsive disorder; schizophrenia;
 KW autism; neurodegenerative disorder.
 XX
 OS Homo sapiens.
 PN WO200229051-A2.
 PD 11-APR-2002.
 PF 04-OCT-2001; 2001WO-EP11443.
 PR 06-OCT-2000; 2000US-238043P.
 XX (FARB) BAYER AG.
 PA Liou J;
 PI
 PS WPI; 2002-362602/39.
 XX
 PT Polynucleotides encoding secretin receptor-like G-protein Coupled
 PT Receptors, useful for preventing, diagnosing and treating urinary
 PT incontinence, benign prostate hyperplasia, obesity, or hypertension -
 XX
 PS Disclosure; Fig 3; 113pp; English.
 XX
 CC The present invention describes a human secretin receptor-like G protein-
 CC coupled receptor (GPCR) (I). (I) has uropathic, cytosolic, anorectic,
 CC antidiabetic, osteopathic, tranquilizer, antidepressant, hypotensive,
 CC antimigraine, neuroleptic, nootropic and antiemetic activities. (I) and
 CC the polynucleotide encoding it (II) can be used in gene therapy,
 CC antisense therapy, protein therapy and vaccine production. (I) and (II)
 CC can be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate secretin receptor-like GPCR expression.
 CC Disorders that may be prevented, diagnosed and/or treated by (I) and
 CC (II) include, for example urinary incontinence, benign prostate
 CC hyperplasia, obesity, or a disease related to obesity, cancer,
 CC diabetes, osteoporosis, anxiety, depression, hypertension, migraine,
 CC compulsive disorder, schizophrenia, autism, a neurodegenerative
 CC disorder or cancer chemotherapy-induced vomiting. Human secretin
 CC receptor-like GPCR is located to chromosome 6. The present sequence
 CC represents a protein given in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 440 AA;
 Query Match 3.5%; Score 19; DB 23; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 169 FRLHCTRNTHMHLFVSP 187
 Db 167 FRLHCTRNTHMHLFVSP 185
 RESULT 22
 ABB81912
 ID ABB81912 standard; Protein; 440 AA.
 AC ABB81912;
 DT 04-MAR-2003 (first entry)
 XX
 DE Human secretin receptor protein SEQ ID NO:310.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer.

XX Homo sapiens.

OS WO200261087-A2.

PN 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US50107.

FF 19-DEC-2000; 2000US-257144P.

PR (LIFE-) LIFESPAN BIOSCIENCES INC.

PA Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

DR N-PSDB; AB242760.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases -

PS Disclosure; Fig 1; 523pp; English.

CC The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related diseases, immunological-related diseases, cell
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 440 AA;

Query Match 3.5%; Score 19; DB 24; Length 440;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNHYHMHFLVFSF 187

DB 167 FRRLHCTRNHYHMHFLVFSF 185

RESULT 23

AAR30187

ID AAR30187 standard; Protein; 449 AA.

XX AAR30187;
 AC 25-MAR-2003 (updated)
 DT 28-APR-1993 (first entry)
 DD Secretin receptor.
 DE Rat; rat/mouse hybridoma; NG 108-15.
 KW Rattus rattus.
 OS
 PH Key Location/Qualifiers
 FT Peptide /note= "signal peptide"
 FT Protein /note= "mature secretin receptor"
 FT Modified-site 72 /note= "potential N-glycosylation site"
 FT Modified-site 100 /note= "potential N-glycosylation site"
 FT Modified-site 106 /note= "potential N-glycosylation site"
 FT Modified-site 128 /note= "potential N-glycosylation site"
 FT Modified-site 291 /note= "potential N-glycosylation site"
 FT Domain 144..165 /note= "transmembrane domain"
 FT Domain 175..194 /note= "transmembrane domain"
 FT Domain 217..240 /note= "transmembrane domain"
 FT Domain 254..276 /note= "transmembrane domain"
 FT Domain 294..317 /note= "transmembrane domain"
 FT Domain 343..362 /note= "transmembrane domain"
 FT Domain 374..394 /note= "transmembrane domain"
 XX WO9221754-A1.
 PN 10-DEC-1992.
 PD 05-JUN-1992; 92WO-JP00728.
 PF 07-JUN-1991; 91JP-0163946.
 PR (OSAB-) OSAKA BIOSCIENCE INST.
 XX Ishihara T, Nagata S, Takahashi K;
 WPI; 1992-433652/52.
 DR N-PSDB; AAQ33018.
 XX DNA coding for secretin receptor - is expressed in COS cells and
 PT produces a receptor protein for research and clinical use
 PS Claim 2; Fig 1; 44pp; Japanese.
 CC The secretin receptor was encoded by a DNA sequence of rat origin,
 CC contained in rat/mouse hybridoma NG108-15. The DNA sequence was
 CC obtd. from a cDNA library derived from NG108-15 cells. Expression
 CC in a suitable host allows prodn. of the receptor protein. The
 CC secretin receptor protein encoded by this gene may be used in basic
 CC research and in clinical tests, and is available in high yield.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 449 AA;

Query Match

3.5%; Score 19; DB 13; Length 449;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNTHMLFVSF 187
|||||
Db 167 FRLHCTRNTHMLFVSF 185

RESULT 24

ABP82551
ID ABP82551 standard; Peptide; 18 AA.

XX AC ABP82551;

XX DT 04-MAR-2003 (first entry)

XX DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1224.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX OS Homo sapiens.

XX PN WO200261087-A2.

XX PD 08-AUG-2002.

XX PF 19-DEC-2001; 2001WO-US50107.

XX PR 19-DEC-2000; 2000US-257144P.

XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burmer GC, Roush CL, Brown JP;

XX DR WPI; 2003-046718/04.

XX PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases

XX PS Claim 1; Fig 2; 523pp; English.

XX CC The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,

CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABP82553 to ABP82869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.

SQ Sequence 18 AA;

Query Match 3.3%; Score 18; DB 24; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e-10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 KAKVQCELNITAIQEGE 60

Db 1 KAKVQCELNITAIQEGE 18

RESULT 25

AA96985

ID AA96985 standard; Protein; 324 AA.

XX AC AA96985;

XX DT 19-DEC-2000 (first entry)

XX DE Tethered PTH-1 receptor, r-del-Nt/Ct.

XX KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;

XX KW PTH-1 receptor; resorption; remodeling; r-delta-Nt/Ct;

XX KW tethered receptor; osteoporosis.

XX OS Chimeric - Rattus sp.

XX OS Synthetic.

XX PN WO200039278-A2.

XX PD 06-JUL-2000.

XX PF 30-DEC-1999; 99WO-US311108.

XX PR 31-DEC-1998; 98US-0114577.

XX PA (GARD/) GARDELLA T J.

XX PA (KRON/) KRONENBERG H M.

XX PA (POTT/) POTTS J T.

XX PA (JUEP/) JUEPPNER H.

XX PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX DR WPI; 2000-452384/39.

XX DR N-PSDB; AAA51734.

XX PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass

XX PS Claim 22; Fig 10; 119pp; English.

XX CC Compounds of the structure or formula S-(L) n-B, R_1-S-(L) n-R or
CC S-(L) n-R, are new. S is an amino terminal signaling functional domain
CC of parathyroid hormone (PTH); L is a linker molecule present n times
CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
CC R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
CC receptor sequence. The new compounds are used for treating mammalian
CC conditions characterized by decreases in bone mass, determining rates of
CC bone reformation, bone resorption and/or bone remodeling, treating
CC diseases and disorders associated with decreased tether activity,
CC increasing CAMP in a mammalian cell having PTH-1 receptors, or screening
CC for a peptide or non-peptide PTH (claimed). The new compound can be
CC administered by inhalation unlike the large native PTH or PTHrp which
CC avoids the need for regular injections to treat osteoporosis.

XX

SQ Sequence 324 AA;

Query Match 3.3%; Score 18; DB 21; Length 324;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 134 YFLATNYWILVEGLYLH 151
 |||||

RESULT 26
 AAY96984
 ID AAY96984 standard; Protein; 335 AA.
 XX AC AAY96984;
 XX DT 31-OCT-2000 (first entry)
 XX DE Tethered PTH-1 receptor, TetherIC.
 XX KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
 XX KW PTH-1 receptor; resorption; remodeling; tetherIC; osteoporosis.
 XX OS Chimeric - Rattus sp.
 XX OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..23 /label= PTH-1_receptor_signal_sequence
 FT Peptide 24..32
 FT Peptide /label= PTH_residues_1-9
 FT Peptide 33..36 /label= linker
 FT Protein 37..335
 FT /label= PTH-1_receptor
 FT /note= "residue 182 to 480"
 XX WO200039278-A2.
 XX PD 06-JUL-2000.
 XX PF 30-DEC-1999; 99WO-US31108.
 XX PR 31-DEC-1998; 98US-0114577.
 XX (GARD/) GARDELLA T J.
 XX (KRON/) KRONENBERG H M.
 XX (PORT/) POTTS J T.
 XX (JUEP/) JUEPPNER H.
 PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
 DR WPI; 2000-452384/39.
 DR N-PSDB; AAA51733.
 XX New compound comprising an amino terminal signaling functional domain
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for
 PT treating mammalian conditions characterized by decreases in bone mass
 PS Claim 22; Fig 9; 119pp; English.
 CC Compounds of the structure or formula S-(L)_n-B, R₁-S-(L)_n-R or
 CC S-(L)_n-R, are new. S is an amino terminal signaling functional domain
 CC of parathyroid hormone (PTH); L is a linker molecule present n times
 CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
 CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34);
 CC R₁ is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
 CC receptor sequence. The new compounds are used for treating mammalian
 CC conditions characterized by decreases in bone mass, determining rates of
 CC bone reformation, bone resorption and/or bone remodeling, treating
 CC diseases and disorders associated with decreased tetherIC activity,
 CC increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
 CC for a peptide or non-peptide PTH (claimed). The new compound can be
 CC administered by inhalation unlike the large native PTH or PTHrP which
 CC avoids the need for regular injections to treat osteoporosis.

CC for a peptide or non-peptide PTH (claimed). The new compound can be
 CC administered by inhalation unlike the large native PTH or PTHrP which
 CC avoids the need for regular injections to treat osteoporosis.
 XX SQ Sequence 335 AA;
 Query Match 3.3%; Score 18; DB 21; Length 335;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 145 YFLATNYWILVEGLYLH 162
 |||||

RESULT 27
 AAY96987
 ID AAY96987 standard; Protein; 435 AA.
 XX AC AAY96987;
 XX DT 31-OCT-2000 (first entry)
 XX DE Human tethered PTH-1 receptor, hdelNT.
 XX KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
 XX KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
 XX OS Chimeric - Homo sapiens.
 XX OS Synthetic.
 XX WO200039278-A2.
 XX PD 06-JUL-2000.
 XX PF 30-DEC-1999; 99WO-US31108.
 XX PR 31-DEC-1998; 98US-0114577.
 XX (GARD/) GARDELLA T J.
 XX (KRON/) KRONENBERG H M.
 XX (PORT/) POTTS J T.
 XX (JUEP/) JUEPPNER H.
 PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
 DR WPI; 2000-452384/39.
 DR N-PSDB; AAA51736.
 XX New compound comprising an amino terminal signaling functional domain
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for
 PT treating mammalian conditions characterized by decreases in bone mass
 PS Example 4; Fig 18; 119pp; English.
 CC Compounds of the structure or formula S-(L)_n-B, R₁-S-(L)_n-R or
 CC S-(L)_n-R, are new. S is an amino terminal signaling functional domain
 CC of parathyroid hormone (PTH); L is a linker molecule present n times
 CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
 CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34);
 CC R₁ is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
 CC receptor sequence. The new compounds are used for treating mammalian
 CC conditions characterized by decreases in bone mass, determining rates of
 CC bone reformation, bone resorption and/or bone remodeling, treating
 CC diseases and disorders associated with decreased tetherIC activity,
 CC increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
 CC for a peptide or non-peptide PTH (claimed). The new compound can be
 CC administered by inhalation unlike the large native PTH or PTHrP which
 CC avoids the need for regular injections to treat osteoporosis.
 XX SQ Sequence 435 AA;
 Query Match 3.3%; Score 18; DB 21; Length 435;

Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
DB 132 YFLATNYWILVEGLYLH 149

RESULT 28

AAB07529
ID AAB07529 standard; Protein; 435 AA.

XX AC AAB07529;

XX 20-OCT-2000 (first entry)

DE A mutant parathyroid hormone (PTH) receptor designated rdelant.

XX Mutant; parathyroid hormone; PTH; receptor; rdelant;

KW ligand binding domain.

XX Homo sapiens.

XX Key Location/Qualifiers

FH Peptide 1..22

FT /note= "signal peptide"

FT 23..435

FT Protein /note= "mature protein"

XX WO200040698-A1.

XX 13-JUL-2000.

XX 31-DEC-1998; 98WO-US27862.

XX 31-DEC-1998; 98WO-US27862.

XX (GEO) GEN HOSPITAL CORP.

XX Gardella TJ, Kronenberg HM, Potts JT;

XX WPI; 2000-465971/40.

XX N-PSDB; AAA58932.

XX New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a deletion of the extracellular amino-terminus ligand binding domain, useful in screening assays for identifying agonists and antagonists of PTH receptor activity -

XX Claim 17; Fig 1; 81pp; English.

XX The present sequence represents a mutant parathyroid hormone (PTH) receptor, designated rdelant. The polypeptide is characterized by a deletion of the extracellular amino-terminus ligand binding domain. The receptor has a minimal domain for ligand binding and is, therefore, useful in screening assays designed for the identification of agonists and antagonists of PTH receptor activity.

XX Sequence 435 AA;

Query Match 3.3%; Score 18; DB 21; Length 435;

Best Local Similarity 100.0%; Pred. No. 2.2e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262

DB 134 YFLATNYWILVEGLYLH 151

RESULT 29

AY96983

ID AY96983 standard; Protein; 446 AA.

XX AY96983;

XX 31-OCT-2000 (first entry)

XX Tethered PTH-1 receptor, Tether1.

XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;

KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.

XX Chimeric - Rattus sp.

XX Synthetic.

XX Key Location/Qualifiers

FH Peptide 1..23

FT /label= PTH-1_receptor_signal_sequence

FT Peptide 24..32

FT /label= PTH_residues_1-9

FT Peptide 33..36

FT /label= linker

FT Protein 37..446

FT /label= PTH-1_receptor

FT /note= "residue 182 to end"

XX WO200039278-A2.

XX 06-JUL-2000.

XX 30-DEC-1999; 99WO-US31108.

XX 31-DEC-1998; 98US-0114577.

XX (CARD/) GARDELLA T J.

XX (KRON/) KRONENBERG H M.

XX (POTT/) POTTS J T.

XX (JUEP/) JUEPPNER H.

XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-452384/39.

XX N-PSDB; AAA51732.

XX New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass

XX Claim 22; Fig 7; 119pp; English.

XX Compounds of the structure or formula S-(L) n-B, R_1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrp which avoids the need for regular injections to treat osteoporosis.

XX Sequence 446 AA;

Query Match 3.3%; Score 18; DB 21; Length 446;

Best Local Similarity 100.0%; Pred. No. 2.3e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262

DB 145 YFLATNYWILVEGLYLH 162

RESULT 30
 ID AAY96986
 XX AAY96986 standard; Protein; 448 AA.
 AC AAY96986;
 XX 31-OCT-2000 (first entry)
 XX Human tethered PTH-1 receptor, Tether1.
 XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
 XX PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
 XX Chimeric - Homo sapiens.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= Signal sequence
 FT /note= "Human PTH-1 receptor residues 1-23"
 FT Peptide 24..32
 FT /label= PTH(1-9)
 FT Peptide 33..36
 FT /label= Linker
 FT Protein 37..448
 FT /label= PTH-1_receptor
 FT /note= "Human PTH-1 receptor residues 182-593"
 XX WO200039278-A2.
 PN 06-JUL-2000.
 PD 30-DEC-1999; 99WO-US31108.
 XX 31-DEC-1998; 98US-0114577.
 XX (GARD/) GARDELLA T J.
 XX (KRON/) KRONENBERG H M.
 XX (POTT/) POTTS J T.
 XX (JUEP/) JUEPPNER H.
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
 XX WPI; 2000-452384/39.
 XX N-PSDB; AAA51735.
 XX New compound comprising an amino terminal signaling functional domain
 XX linked to a carboxy-terminal binding portion of parathyroid hormone for
 XX treating mammalian conditions characterized by decreases in bone mass
 XX Example 4; Fig 17; 119pp; English.
 XX Compounds of the structure or formula S-(L) n-B, R_1-S-(L) n-R or
 XX S-(L) n-R, are new. S is an amino terminal signaling functional domain
 XX of parathyroid hormone (PTH); L is a linker molecule present n times
 XX (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
 XX binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
 XX R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
 XX receptor sequence. The new compounds are used for treating mammalian
 XX conditions characterized by decreases in bone mass, determining rates of
 XX bone reformation, bone resorption and/or bone remodeling, treating
 XX diseases and disorders associated with decreased tether1 activity,
 XX increasing CAMP in a mammalian cell having PTH-1 receptors, or screening
 XX for a peptide or non-peptide PTH (claimed). The new compound can be
 XX administered by inhalation unlike the large native PTH or PTHrp which
 XX avoids the need for regular injections to treat osteoporosis.
 XX Sequence 448 AA;
 SQ Query Match 3.3%; Score 18; DB 21; Length 448;
 Best Local Similarity 100.0%; Pred. No. 2.3e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVGLYLH 262
 Db 145 YFLATNYWILVGLYLH 162
 RESULT 31
 ID AAY96988
 XX AAY96988 standard; Protein; 450 AA.
 AC AAY96988;
 XX 31-OCT-2000 (first entry)
 XX Human tethered PTH-1 receptor, Tether-R11.
 XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
 XX PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.
 XX Chimeric - Homo sapiens.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= Signal sequence
 FT /note= "Human PTH-1 receptor residues 1-23"
 FT Peptide 24..34
 FT /label= PTH(1-11)
 FT Peptide 35..38
 FT /label= Linker
 FT Protein 39..450
 FT /label= PTH-1_receptor
 FT /note= "Human PTH-1 receptor residues 182-593"
 XX WO200039278-A2.
 PN 06-JUL-2000.
 PD 30-DEC-1999; 99WO-US31108.
 XX 31-DEC-1998; 98US-0114577.
 XX (GARD/) GARDELLA T J.
 XX (KRON/) KRONENBERG H M.
 XX (POTT/) POTTS J T.
 XX (JUEP/) JUEPPNER H.
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
 XX WPI; 2000-452384/39.
 XX N-PSDB; AAA51737.
 XX New compound comprising an amino terminal signaling functional domain
 XX linked to a carboxy-terminal binding portion of parathyroid hormone for
 XX treating mammalian conditions characterized by decreases in bone mass
 XX Example 4; Fig 19; 119pp; English.
 XX Compounds of the structure or formula S-(L) n-B, R_1-S-(L) n-R or
 XX S-(L) n-R, are new. S is an amino terminal signaling functional domain
 XX of parathyroid hormone (PTH); L is a linker molecule present n times
 XX (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
 XX binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
 XX R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
 XX receptor sequence. The new compounds are used for treating mammalian
 XX conditions characterized by decreases in bone mass, determining rates of
 XX bone reformation, bone resorption and/or bone remodeling, treating
 XX diseases and disorders associated with decreased tether1 activity,
 XX increasing CAMP in a mammalian cell having PTH-1 receptors, or screening
 XX for a peptide or non-peptide PTH (claimed). The new compound can be
 XX administered by inhalation unlike the large native PTH or PTHrp which
 XX avoids the need for regular injections to treat osteoporosis.

SQ Sequence 450 AA;

Query Match 3.3%; Score 18; DB 21; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.3e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262
 Db 147 YFLATNYWILVEGLYH 164

RESULT 32
 AAY99600
 ID AAY99600 standard; Protein; 536 AA.
 XX
 AC AAY99600;
 XX
 DT 27-OCT-2000 (first entry)
 DE Zebrafish parathyroid hormone type-1 receptor PTH1R.
 XX
 KW Zebrafish; parathyroid hormone type-1 receptor; PTH1R;
 development disorder; physiological disorder; neurological disorder.
 XX
 OS Brachydanio rerio.
 XX
 FN WO200032775-A1.
 XX
 PD 08-JUN-2000.
 XX
 PF 30-NOV-1999; 99WO-US28207.
 XX
 PR 30-NOV-1998; 98US-0110457.
 XX
 PA (JUEP/) JUEPPNER H.
 (RUBI/) RUBIN D A.
 XX
 PI Jueppner H, Rubin DA;
 XX
 DR WPI; 2000-412323/35.
 DR N-PSDB; AAA49625.
 XX
 PT New nucleic acids encoding parathyroid hormone receptors PTH1R and
 PTH3R, useful for treating diseases or disorders associated with
 PT impaired receptor functions comprises a specific nucleotide sequence -
 XX
 PS Claim 17; Fig 2A; 111pp; English.
 XX
 CC The present sequence is the parathyroid hormone type-1 receptor
 CC (PTH1R) from the zebrafish. Its coding sequence was obtained by
 CC sequencing a cDNA clone. The gene and protein can be used to detect
 CC diseases in man where the receptor is either overexpressed or
 CC underexpressed, and they can be used to treat these diseases, which may
 CC be developmental, physiological or neurological disorders. They can also
 CC be used to identify agonists and antagonists which can be used in a
 CC similar manner. In addition, the gene can be used for chromosome
 CC identification.
 XX
 SQ Sequence 536 AA;

Query Match 3.3%; Score 18; DB 21; Length 536;
 Best Local Similarity 100.0%; Pred. No. 2.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRYNHMLF 184
 Db 167 GYFRLHCTRYNHMLF 184

RESULT 33
 AAY90230
 ID AAY90230 standard; Protein; 536 AA.
 XX

AC AAY90230;

XX 29-AUG-2000 (first entry)

XX Zebrafish PTH1R receptor protein sequence.

DE Zebrafish; PTH1R receptor; PTH3R receptor; diagnosis; cancer;
 parathyroid hormone type 1 receptor; parathyroid hormone type 3 receptor.
 XX
 OS Brachydanio rerio.
 XX
 PN WO200032771-A1.
 XX
 PD 08-JUN-2000.
 XX
 PF 28-MAY-1999; 99WO-US11883.
 XX
 PR 30-NOV-1998; 98US-0110467.
 XX
 PA (JUEP/) JUEPPNER H.
 (RUBI/) RUBIN D A.
 XX
 PI Jueppner H, Rubin DA;
 XX
 DR WPI; 2000-412319/35.
 DR N-PSDB; AAA30828.
 XX
 PT Novel zebrafish parathyroid hormone/parathyroid hormone related peptide
 PT receptor 3 and isolated nucleic acid encoding zebrafish parathyroid
 PT hormone receptor 1 for treating disorders associated with receptor
 PT function -
 XX
 PS Claim 17; Fig 2a; 111pp; English.
 XX
 CC This sequence is a parathyroid hormone receptor type 1 (PTH1R)
 CC receptor protein of the invention. The invention also relates to a PTH3R
 CC receptor protein. Antagonists of PTH1R or PTH3R can be used for the
 CC treatment of diseases associated with an increase in PTH1R or PTH3R
 CC activity, respectively. The peptides are used for diagnosis or prognosis
 CC of diseases and disorders associated with PTH3R or PTH1R, such as cancer.
 CC The polypeptides can be used as a molecular weight markers on sodium
 CC dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or
 CC on molecular sieve gel filtration columns. Antigenic epitope-bearing
 CC peptides and polypeptides are useful to raise antibodies, including
 CC monoclonal antibodies, that bind specifically to a polypeptide. The
 CC peptides are useful during diagnosis of diseases and disorders in
 CC mammals involving PTH1R or PTH3R receptor expression or function.
 CC Mutations that affect PTH1R or PTH3R sequence and/or expression levels
 CC of PTH1R or PTH3R could be diagnostic for patients with disease or
 CC disorders of a developmental, physiological or neurological nature. The
 CC nucleic acid molecules are valuable for chromosome identification. The
 CC mapping of DNAs to chromosomes is an important first step in
 CC correlating those sequences with genes associated with disease.
 XX
 SQ Sequence 536 AA;

Query Match 3.3%; Score 18; DB 21; Length 536;
 Best Local Similarity 100.0%; Pred. No. 2.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRYNHMLF 184
 Db 167 GYFRLHCTRYNHMLF 184

RESULT 34
 AAR27706
 ID AAR27706 standard; Protein; 591 AA.
 XX
 AC AAR27706;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-MAR-1993 (first entry)

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XX DE Rat bone PTH/PTHrP receptor clone R15B prod.
XX KW Parathyroid hormone; related protein; calcium; antagonist;
XX KW antibodies; hypercalcaemia.
XX OS Rattus rattus.
XX PN WO9217602-A1.
XX PD 15-OCT-1992.
XX PF 06-APR-1992; 92WO-US02821.
XX PR 05-APR-1991; 91US-0681702.
XX PR 06-APR-1992; 92US-0864475.
XX PA (GEO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
XX PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
XX PI Segre GV;
XX DR WPI; 1992-366271/44.
XX DR N-PSDB; AAQ29606.
XX PT New DNA encoding parathyroid hormone receptor, DNA and antibodies
XX PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
XX PT and treatment of tumours
XX PS Claim 20; Fig 3; 91pp; English.
XX CC The rat bone parathyroid hormone/parathyroid hormone related
XX CC protein (PTH/PTHrP) receptor protein sequence was deduced from
XX CC clone R15B obd. by screening a rat osteosarcoma (ROS) cell cDNA library
XX CC to isolate those expressing functionally intact PTH/PTHrP receptor
XX CC proteins, performed according to Gearing et al., (EMBO J. 8: 3676,
XX CC 1989), by identifying colonies capable of binding a suitable radio-
XX CC labelled ligand. The protein may be used in a therapeutic compsn. to
XX CC inhibit activation of PTH or PTHrP and thus reduce the level of calcium
XX CC in the blood. Cpdns. capable of competing with PTH or PTHrP for binding
XX CC can be identified using the protein and DNAs homologous to PTH DNA can
XX CC be identified using fragments of the clone as probes. The sequence
XX CC may be used for the prodn. of antibodies useful for the treatment,
XX CC classification, prognosis and/or treatment of disorders related to
XX CC the interaction between a cell receptor and a ligand such as in
XX CC hypercalcaemia. See also AAR27704-16.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 591 AA;

Query Match 3.3%; Score 18; DB 13; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262
   |||||
Db 290 YFLATNYWILVEGLYH 307

RESULT 35
AAR92277
ID AAR92277 standard; Protein; 591 AA.
XX AC AAR92277;
XX XX
DT 25-MAR-2003 (updated)
DT 18-MAY-1996 (first entry)
XX DE Rat bone PTH/PTHrP receptor.
XX KW Parathyroid hormone; receptor; parathormone; PTH;
KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
KW hypercalcaemia; hypocalcaemia; cancer.

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XX OS Rattus sp.
XX FH Key
XX FT Location/Qualifiers
XX FT 1..192
XX FT /label= Extracellular_region
XX FT 193..211
XX FT /label= Transmembrane_region
XX FT 212..221
XX FT /label= Intracellular_region
XX FT 222..240
XX FT /label= Transmembrane_region
XX FT 241..299
XX FT /label= Extracellular_region
XX FT 300..316
XX FT /label= Transmembrane_region
XX FT 317..325
XX FT /label= Intracellular_region
XX FT 326..342
XX FT /label= Transmembrane_region
XX FT 343..364
XX FT /label= Extracellular_region
XX FT 365..383
XX FT /label= Transmembrane_region
XX FT 384..408
XX FT /label= Intracellular_region
XX FT 409..428
XX FT /label= Transmembrane_region
XX FT 429..444
XX FT /label= Intracellular_region
XX FT 445..463
XX FT /label= Transmembrane_region
XX FT 464..591
XX FT /label= Intracellular_region
XX PN US5494806-A.
XX PD 27-FEB-1996.
XX PF 06-APR-1992; 92US-0864475.
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PA (GEO ) GEN HOSPITAL CORP.
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX DR WPI; 1996-139028/14.
XX DR N-PSDB; AAT15947.
XX PT DNA encoding vertebrate parathyroid hormone receptor - useful for
XX PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
XX PT cancer etc.
XX PS Claim 1; Fig 3A-3E; 64pp; English.
XX CC A rat parathyroid hormone/parathyroid hormone-related protein
XX CC (PTH/PTHrP) receptor (AAR92277) is encoded by cDNA clone R15B
XX CC (AAT15947) isolated from a rat osteosarcoma ROS 17/2.8 cDNA library.
XX CC The receptor a G-protein linked receptor having 7 transmembrane
XX CC domains. It induces an increase in intracellular cAMP and calcium
XX CC upon challenge with PTH or PTHrP. Recombinant receptor can be
XX CC produced in vector/host cell systems and used in the treatment,
XX CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia,
XX CC to screen for (antagonists and to raise antibodies. Host cells
XX CC expressing the receptor are used for diagnostic measurement of PTH
XX CC serum levels.
XX CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 591 AA;

```

Query Match 3.3%; Score 18; DB 17; Length 591;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 290 YFLATNYWILVEGLYLH 307

RESULT 36

AAW73316
 ID AAW73316 standard; Protein; 591 AA.

AC AAW73316;

DT 08-FEB-1999 (first entry)

DE Parathyroid hormone receptor R15B.

XX Parathyroid hormone receptor; PTH receptor; antibody; therapy;

KW PTH-related hypercalcaemia; rat.

OS Rattus sp.

PN US5840853-A.

PD 24-NOV-1998.

XX 06-JUN-1995; 95US-0471494.

PR 06-APR-1992; 92US-0864475.

PR 05-APR-1991; 91US-0681702.

PR 06-JUN-1995; 95US-0471494.

XX (GEHO) GEN HOSPITAL CORP.

PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;

PI Schipani E, Segre GV;

DR WPI; 1999-034124/03.

DR N-PSDB; AAV08390.

XX Antibody to parathyroid hormone receptor - for diagnostic or

PT therapeutic use

PS Claim 6; Fig 3; 63pp; English.

XX This sequence represents the rat parathyroid hormone (PTH) receptor
 CC R15B, which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat or
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.

XX Sequence 591 AA;

Query Match 3.3%; Score 18; DB 20; Length 591;

Best Local Similarity 100.0%; Pred. No. 2.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 290 YFLATNYWILVEGLYLH 307

RESULT 37

AAR92278
 ID AAR92278 standard; Protein; 593 AA.

XX AAR92278;

XX 25-MAR-2003 (updated)

DT 18-MAY-1996 (first entry)

XX

DE Human kidney PTH/PTHrP receptor.

XX

KW Parathyroid hormone; receptor; parathormone; PTH;

KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;

XX hypercalcaemia; hypocalcaemia; cancer.

OS

XX Homo sapiens.

PN US5494806-A.

PD 27-FEB-1996.

XX 06-APR-1992; 92US-0864475.

PR 06-APR-1992; 92US-0864475.

PR 05-APR-1991; 91US-0681702.

XX (GEHO) GEN HOSPITAL CORP.

XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;

PI Schipani E, Segre GV;

XX WPI; 1996-139028/14.

DR N-PSDB; AAT15948.

XX DNA encoding vertebrate parathyroid hormone receptor - useful for
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
 PT cancer etc.

XX Claim 1; Fig 6A-6G; 64pp; English.

XX A human parathyroid hormone/parathyroid hormone-related protein
 CC (PTH/PTHrP) receptor (AAR92278) is encoded by cDNA clone HK-1
 CC (AAT15948) isolated from a human kidney cDNA library. The receptor
 CC induces an increase in intracellular cAMP and intracellular free
 CC calcium when challenged by PTH or PTHrP. Recombinant receptor can
 CC be produced in vector/host cell systems and used in the treatment,
 CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to
 CC screen for (ant)agonists and to raise antibodies. Host cells
 CC expressing the receptor can be used for diagnostic measurement of
 CC PTH serum levels.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 593 AA;

Query Match 3.3%; Score 18; DB 17; Length 593;

Best Local Similarity 100.0%; Pred. No. 2.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 290 YFLATNYWILVEGLYLH 307

RESULT 38

AAW73317

ID AAW73317 standard; Protein; 593 AA.

XX AAW73317;

XX 08-FEB-1999 (first entry)

DE Human Parathyroid hormone receptor.

XX

KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;

KW PTH-related hypercalcaemia; human.

XX Homo sapiens.

PN US5840853-A.

XX 24-NOV-1998.

PD

XX PF 06-JUN-1995; 95US-0471494.
 XX PR 06-APR-1992; 92US-0864475.
 PR 05-APR-1991; 91US-0681702.
 PR 06-JUN-1995; 95US-0471494.
 XX PA (GEO) GEN HOSPITAL CORP.
 XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX DR WPI; 1999-034124/03.
 DR N-PSDB; AAV08391.
 XX PT Antibody to parathyroid hormone receptor - for diagnostic or
 PT therapeutic use
 XX PS Claim 7; Fig 6; 63pp; English.
 XX CC This sequence represents the human parathyroid hormone (PTH) receptor
 CC which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat or
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.
 XX CC
 XX SQ Sequence 593 AA;
 Query Match 3.3%; Score 18; DB 20; Length 593;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 YFLATNYWILVEGLYLH 262
 DB 290 YFLATNYWILVEGLYLH 307
 |||||
 |||||
 RESULT 39
 ABB56385
 ID ABB56385 standard; Protein; 593 AA.
 AC ABB56385;
 XX DT 18-FEB-2002 (first entry)
 XX DE Non-endogenous human GPCR protein, SEQ ID NO: 563.
 XX KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 KW constitutively activated GPCR; agonist; disease.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200177172-A2.
 XX PD 18-OCT-2001.
 XX PF 05-APR-2001; 2001WO-US11098.
 XX PR 07-APR-2000; 2000US-195747P.
 XX PA (AREN-) ARENA PHARM INC.
 XX PI Lehmann-Bruinsma K, Liaw CW, Lin I;
 XX DR WPI; 2001-648759/74.
 DR N-PSDB; ABI98021.
 XX PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with
 PT versions of GPCRs -

PS Claim 1; Page 364-366; 394pp; English.
 XX CC The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous
 CC constitutively activated versions of known GPCRs are used in the
 CC invention for the direct identification of candidate compounds as
 CC receptor agonists, inverse agonists or partial agonists. Such
 CC agonists are useful as therapeutic agents for diseases or disorders
 CC associated with GPCRs. The present sequence is a non-endogenous
 CC version of a known human GPCR.
 XX SQ Sequence 593 AA;
 Query Match 3.3%; Score 18; DB 22; Length 593;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 YFLATNYWILVEGLYLH 262
 DB 290 YFLATNYWILVEGLYLH 307
 |||||
 |||||
 RESULT 40
 AAB71876
 ID AAB71876 standard; Protein; 593 AA.
 XX AC AAB71876;
 XX DT 03-MAY-2001 (first entry)
 XX DE Human PTHR seven transmembrane domain.
 XX KW Human; parathyroid hormone/parathyroid hormone-related peptide receptor;
 KW PTHR; h15571; immunomodulatory; vascular; hepatic; antiasthma;
 KW antimicrobial; antiinflammatory; immunosuppressive; Gene therapy;
 KW vaccine; G-protein coupled receptor; GPCR; liver fibrosis;
 KW respiratory disorder; infection; chronic inflammatory disease;
 KW organ-specific autoimmunity; graft rejection; cystic fibrosis.
 XX OS Homo sapiens.
 XX PN WO200109328-A1.
 XX PD 08-FEB-2001.
 XX PF 03-AUG-2000; 2000WO-US21278.
 XX PR 03-AUG-1999; 99US-0146916.
 PR 29-FEB-2000; 2000US-0515781.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Hodge MR, Lloyd C, Weich NS;
 XX DR WPI; 2001-138653/14.
 XX PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
 XX PS Disclosure; Fig 2; 145pp; English.
 XX CC The present sequence is a human G-protein coupled receptor (GPCR) used
 CC for comparison with the seven transmembrane domain of a novel GPCR
 CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate GPCR expression. Such diseases include immune,
 CC haematological, fibrotic, hepatic and respiratory disorders including
 CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
 CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
 CC graft rejection, graft versus host disease, cystic fibrosis and, in
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
 CC in the production of antibodies against GPCR and in assays to identify

CC modulators (agonists and antagonists) of GPCR expression and activity.
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
 CC used as diagnostic agents for detecting the presence of GPCR
 CC polypeptides in samples.
 XX
 SQ Sequence 593 AA;

Query Match 3.3%; Score 18; DB 22; Length 593;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 |||||
 DB 290 YFLATNYWILVEGLYLH 307

RESULT 41

ABP81872
 ID ABP81872 standard; Protein; 593 AA.

XX
 AC ABP81872;

DT 04-MAR-2003 (first entry)

DE Human parathyroid hormone receptor 1 protein SEQ ID NO:229.

XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

OS Homo sapiens.

XX
 PN W0200261087-A2.

XX
 PD 08-AUG-2002.

XX
 PF 19-DEC-2001; 2001WO-US50107.

XX
 PR 19-DEC-2000; 2000US-257144P.

XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX
 PI Burner GC, Roush CL, Brown JP;

XX
 DR WPI; 2003-046719/04.

XX
 DR N-PSDB; ABZ42719.

XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -
 XX

PS Disclosure; Fig 1; 523pp; English.

XX
 CC The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnoses. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

SQ Sequence 593 AA;

Query Match 3.3%; Score 18; DB 24; Length 593;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 |||||
 DB 290 YFLATNYWILVEGLYLH 307

RESULT 42

ABG73825
 ID ABG73825 standard; Protein; 595 AA.

XX
 AC ABG73825;

DT 02-APR-2003 (first entry)

DE Canine parathyroid hormone 1 receptor, PTH1.

XX
 KW dog; parathyroid hormone 1; receptor; PTH1; hypercalcaemia; PTHrP;
 KW hypocalcaemia; PTH mediated hypercalcaemia;
 KW parathyroid hormone related protein; PTHrP mediated hypercalcaemia;
 KW local osteolytic hypercalcaemia; malignancy-related hypercalcaemia;
 KW G-protein coupled receptor family.

XX
 OS Canis sp.

XX
 PF Key Location/Qualifiers
 XX Region 250..262
 XX /note= "Anti-PTH1 antibody epitope region"

XX
 FT US2002146777-A1.

XX
 PD 10-OCT-2002.

XX
 PF 30-AUG-2001; 2001US-0943446.

XX
 PR 30-AUG-2000; 2000US-229170P.

XX
 PA (CAST/) CASTLEBERRY T A.

XX
 PA (LJBB/) LU B.

XX
 PA (OWEN/) OWEN T A.

XX
 PA (SMOC/) SMOCK S L.

XX
 PI Castleberry TA, Lu B, Owen TA, Smock SL;

XX
 DR WPI; 2003-174177/17.

XX
 DR N-PSDB; ABX15515.

XX
 PT Isolated proteinaceous molecule having canine parathyroid hormone 1
 PT receptor activity used, e.g. for veterinary purposes to treat dogs,
 PT comprises naturally occurring canine peptide -

XX
 PS Claim 1; Fig 1; 17pp; English.

XX

CC The invention relates to an isolated proteinaceous molecule having canine
CC parathyroid hormone 1 receptor (PTHr) activity, comprising naturally
CC occurring canine peptide or naturally occurring canine peptide having one
CC or more conservative substitutions. PTHr is a member of the G-protein
CC coupled receptor family. The molecules can be used, e.g. for
CC veterinary purposes to treat dogs. The polypeptides are useful for the
CC diagnosis, classification, prognosis, and/or treatment of canine
CC disorders which may be characterised as related to the interaction
CC between a cell receptor and its specific ligand, e.g. some forms of
CC hypercalcaemia and hypocalcaemia. The polypeptides are useful for
CC distinguishing between hypercalcaemic conditions e.g. PTH mediated
CC hypercalcaemia, parathyroid hormone related protein (PTHrP) mediated
CC hypercalcaemia, hypercalcaemia which does not involve these factors
CC (local osteolytic hypercalcaemia) and malignancy-related hypercalcaemia.
CC Large quantities of proteinaceous molecules having canine PTHr activity
CC can be produced. The present sequence represents the amino acid sequence
CC of canine parathyroid hormone 1 receptor, PTHr.

SQ Sequence 595 AA;
Query Match 3.3%; Score 18; DB 24; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|||||
Db 289 YFLATNYWILVEGLYLH 306
|||||

RESULT 43
AAR27707
ID AAR27707 standard; Protein; 614 AA.

AC AAR27707;
XX
XX
DT 25-MAR-2003 (updated)
DT 16-MAR-1993 (first entry)
XX
XX
DE Human kidney PTH/PTHrP receptor.

XX
XX
KW Parathyroid hormone; related protein; calcium; antagonist;
KW antibodies; hypercalcaemia.

OS Homo sapiens.

PN WO9217602-A1.

XX
PD 15-OCT-1992.

XX
PF 06-APR-1992; 92WO-US02821.

XX
PR 05-APR-1991; 91US-0681702.

XX
PR 06-APR-1992; 92US-0864475.

PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani B;
PI Segre GV;

XX
DR WPI; 1992-366271/44.

XX
DR N-PSDB; AAQ29607.

XX
XX
PT New DNA encoding parathyroid hormone receptor, DNA and antibodies
PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours

XX
PS Claim 22; Fig 6; 91pp; English.

XX
CC The protein sequence was deduced from the cDNA sequence obtd by
CC screening a human kidney oligo dt-primed cDNA library in lambda
CC gt10 and a genomic library of human placental DNA in EMBL3 with a
CC probe comprising most of the coding sequence of rat bone parathyroid
CC hormone/parathyroid hormone related protein (PTH/PTHrP) receptor

CC protein. The clone encodes a protein which may be used in a
CC therapeutic compen. to inhibit activation of PTH or PTHrP and thus
CC reduce the level of calcium in the blood. Cpd. capable of competing
CC with PTH or PTHrP for binding can be identified using the protein prod.
CC and DNAs homologous to PTH DNA can be identified using fragments of the
CC clone as probes. The sequence may be used for the prodn. of antibodies
CC useful for the treatment, classification, prognosis and/or treatment of
CC disorders related to the interaction between a cell receptor and a
CC ligand such as in hypercalcaemia. See also R27704-16.
CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 614 AA;

Query Match 3.3%; Score 18; DB 13; Length 614;
Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|||||
Db 290 YFLATNYWILVEGLYLH 307
|||||

RESULT 44
ABB79169
ID ABB79169 standard; protein; 447 AA.

XX
AC ABB79169;

XX
DT 07-AUG-2002 (first entry)

XX
DE Carassius auratus VPAC1 receptor protein SEQ ID NO:9.

XX
KW VPAC receptor; vasoactive intestinal peptide receptor; VIP; cytostatic;
KW vasoactive intestinal peptide; muscle mass regulation; antibacterial;
KW immunosuppressive; immunomodulator; antiinflammatory; infection; sepsis;
KW skeletal muscle atrophy; autoimmune disease; infectious disease; cancer;
KW cachexia; chronic inflammation; congestive heart failure; sarcopenia;
KW AIDS; genetic disorder; muscular dystrophy; neurodegenerative disease.

OS Carassius auratus.

XX
PN WO200235240-A2.

XX
XX
PD 02-MAY-2002.

XX
PF 22-OCT-2001; 2001WO-US43882.

XX
PR 23-OCT-2000; 2000US-0694519.

XX
PA (PROC) PROCTER & GAMBLE CO.

XX
PI Isfort RJ, Sheldon RJ;

XX
DR WPI; 2002-471451/50.

XX
PT Identifying candidate compounds for regulating skeletal muscle mass or
PT function by contacting test compound with vasoactive intestinal peptide
PT receptors or cell expressing the receptor -

XX
PS Disclosure; Page 76-77; 87pp; English.

XX
CC The present invention describes a method for identifying candidate
CC compounds (CC) for regulating skeletal muscle mass or function. The
CC method involves contacting a test compound (TC) with a vasoactive
CC intestinal peptide receptors (VPAC) or cell expressing VPAC receptor
CC and determining whether TC binds to VPAC receptor or TC that activates
CC the VPAC receptors, where the TC that binds to or activates VPAC is
CC identified as CC. The method can be used for identifying CC for
CC regulating skeletal mass or function. Other methods from the present
CC invention can be used for: identifying CC that prolong or augment the
CC activation of VPAC receptor or VPAC receptor signal transduction pathway;
CC identifying CC for increasing VPAC receptor expression; identifying CC
CC for increasing the expression of vasoactive intestinal peptide (VIP) or a

CC VIP analogue; increasing skeletal mass or function in a subject; and for
 CC treating skeletal muscle atrophy in a subject. A pharmaceutical
 CC composition comprising a safe and effective amount of a VPAC receptor
 CC agonist can be used for modulating skeletal muscle atrophy which includes
 CC skeletal muscle atrophy induced by disuse due to surgery, bed rest,
 CC broken bones; denervation/nerve damage due to spinal cord injury,
 CC autoimmune disease, infectious disease, glucocorticoid use for unrelated
 CC conditions, sepsis due to infection or other causes, nutrient limitation
 CC due to illness or starvation, cancer, cachexia, chronic inflammation,
 CC AIDS cachexia, COPD, congestive heart failure, sarcopenia and genetic
 CC disorders, e.g., muscular dystrophies, neurodegenerative diseases.
 CC The present sequence represents a VPAC1 receptor which is given
 CC in the exemplification of the present invention.

XX SQ Sequence 447 AA;

Query Match 3.0%; Score 16; DB 23; Length 447;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLFVSF 187
 |||||
 Db 131 LHCTRNVIHMLFVSF 146

RESULT 45

AAR27710
 ID AAR27710 standard; peptide; 19 AA.

XX AC AAR27710;

DT 25-MAR-2003 (updated)
 DT 16-MAR-1993 (first entry)

XX PTH/PTHrP receptor fragment.

XX Parathyroid hormone; related protein; calcium; antagonist;
 KW antibodies; hypercalcaemia; extracellular domain.

XX Synthetic.

XX WO9217602-A1.

XX 15-OCT-1992.

XX 06-APR-1992; 92WO-US02821.

XX 05-APR-1991; 91US-0681702.

XX 06-APR-1992; 92US-0864475.

XX (GEHO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
 PI Segre GV;

XX WPI; 1992-366271/44.

XX New DNA encoding parathyroid hormone receptor, DNA and antibodies
 PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
 PT and treatment of tumours

XX Claim 25; Page 5; 91pp; English.

XX The peptide sequence shown represents an extracellular fragment of
 CC parathyroid hormone/parathyroid hormone related protein
 CC (PTH/PTHrP) receptor protein. The peptide is capable of binding
 CC PTH or PTHrP and acting as an antagonist of these cpds. The
 CC peptide may be used to inhibit activation of PTH or PTHrP and thus
 CC reduce the level of calcium in the blood. Cpds. capable of competing
 CC with PTH or PTHrP for binding can be identified using the protein prod.
 CC and DNAs homologous to PTH DNA can be identified using fragments of the
 CC clone as probes. The sequence may be used for the prodn. of antibodies
 CC useful for the treatment, classification, prognosis and/or treatment of

CC disorders related to the interaction between a cell receptor and a
 CC ligand such as in hypercalcaemia. See also AAR27704-16.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 19 AA;

Query Match 2.6%; Score 14; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYWILVEG 258
 |||||
 Db 6 YFLATNYYWILVEG 19

RESULT 46

AAR92281
 ID AAR92281 standard; Peptide; 19 AA.

XX AC AAR92281;

DT 25-MAR-2003 (updated)
 DT 18-MAY-1996 (first entry)

XX PTH/PTHrP extracellular region fragment RP-3.

XX Parathyroid hormone; receptor; parathormone; PTH;
 KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
 KW hypercalcaemia; hypocalcaemia; cancer.

XX Synthetic.

XX US5494806-A.

XX 27-FEB-1996.

XX 06-APR-1992; 92US-0864475.

XX 06-APR-1992; 92US-0864475.

XX 05-APR-1991; 91US-0681702.

XX (GEHO) GEN HOSPITAL CORP.

XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;

XX WPI; 1996-139028/14.

XX DNA encoding vertebrate parathyroid hormone receptor - useful for
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
 PT cancer etc.

XX Claim 21; Column 3; 64pp; English.

XX Parathyroid hormone (PTH) receptor fragments, including those
 CC (AAR92279-84) based on the PTH extracellular region and those
 CC (AAR92285-87) based on the intracellular domain, are produced by
 CC incorporating encoding DNA sequences into a vector, and
 CC culturing cells transformed by the vector. The peptides can be
 CC used to raise antibodies. The peptides and antibodies are useful
 CC in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and
 CC hypocalcaemia, and can also be used to screen for (ant)agonists
 CC of therapeutic appln.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 19 AA;

Query Match 2.6%; Score 14; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYWILVEG 258
 |||||

Db 6 YFLATNYWILVEG 19

RESULT 47
AAW73320
ID AAW73320 standard; peptide; 19 AA.
XX AC AAW73320;
DT 08-FEB-1999 (first entry)
XX DE Parathyroid hormone receptor fragment RP-3.
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
KW PTH-related hypercalcaemia; opossum; rat; human.
XX OS Synthetic.
XX PN US5840853-A.
XX PD 24-NOV-1998.
XX PF 06-JUN-1995; 95US-0471494.
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PR 06-JUN-1995; 95US-0471494.
XX PA (GEO) GEN HOSPITAL CORP.
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
XX WPI; 1999-034124/03.
XX PT Antibody to parathyroid hormone receptor - for diagnostic or
PT therapeutic use
XX PS Claim 8; Column 19; 63pp; English.
XX CC This sequence is a fragment of a opossum parathyroid hormone (PTH)
CC receptor which is targeted by the antibody of the invention. The antibody
CC of the invention is immunoreactive with naturally occurring human, rat or
CC opossum PTH receptor. The antibody is useful for treating disorders
CC characterised by overstimulation of PTH receptors by their ligand and for
CC the diagnosis of PTH-related hypercalcaemia.
XX SQ Sequence 19 AA;
Query Match 2.6%; Score 14; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 YFLATNYWILVEG 258
Db 6 YFLATNYWILVEG 19
RESULT 48
ABB79166
ID ABB79166 standard; protein; 444 AA.
XX AC ABB79166;
XX DT 07-AUG-2002 (first entry)
XX DE Rana ridibunda VPAC1 receptor protein SEQ ID NO:6.
XX KW VPAC receptor; vasoactive intestinal peptide receptor; VIP; cytostatic;
KW vasoactive intestinal peptide; muscle mass regulatory; antibacterial;
KW immunosuppressive; immunomodulator; antiinflammatory; infection; sepsis;
KW skeletal muscle atrophy; autoimmune disease; infectious disease; cancer;
KW cachexia; chronic inflammation; congestive heart failure; sarcopenia;
KW

KW AIDS; genetic disorder; muscular dystrophy; neurodegenerative disease.
XX Rana ridibunda.
XX PN WO200235240-A2.
XX PD 02-MAY-2002.
XX PF 22-OCT-2001; 2001WO-US43882.
XX PR 23-OCT-2000; 2000US-0694519.
XX PA (PROC) PROCTER & GAMBLE CO.
XX PI Isfort RJ, Sheldon RJ;
XX WPI; 2002-471451/50.
XX PT Identifying candidate compounds for regulating skeletal muscle mass or
PT function by contacting test compound with vasoactive intestinal peptide
PT receptors or cell expressing the receptor -
XX Disclosure; Page 71-73; 87pp; English.
XX CC The present invention describes a method for identifying candidate
CC compounds (CC) for regulating skeletal muscle mass or function. The
CC method involves contacting a test compound (TC) with a vasoactive
CC intestinal peptide receptors (VPAC) or cell expressing VPAC receptor
CC and determining whether TC binds to VPAC receptor or TC that activates
CC the VPAC receptors, where the TC that binds to or activates VPAC is
CC identified as CC. The method can be used for identifying CC for
CC regulating skeletal mass or function. Other methods from the present
CC invention can be used for: identifying CC that prolong or augment the
CC activation of VPAC receptor or VPAC receptor signal transduction pathway;
CC identifying CC for increasing VPAC receptor expression; identifying CC
CC for increasing the expression of vasoactive intestinal peptide (VIP) or a
CC VIP analogue; increasing skeletal mass or function in a subject; and for
CC treating skeletal muscle atrophy in a subject. A pharmaceutical
CC composition comprising a safe and effective amount of a VPAC receptor
CC agonist can be used for modulating skeletal muscle atrophy which includes
CC skeletal muscle atrophy induced by disuse due to surgery, bed rest,
CC broken bones, denervation/nerve damage due to spinal cord injury,
CC autoimmune disease, infectious disease, glucocorticoid use for unrelated
CC conditions, sepsis due to infection or other causes, nutrient limitation
CC due to illness or starvation, cancer, cachexia, chronic inflammation,
CC AIDS cachexia, COPD, congestive heart failure, sarcopenia and genetic
CC disorders, e.g., muscular dystrophies, neurodegenerative diseases.
CC The present sequence represents a VPAC1 receptor which is given
CC in the exemplification of the present invention.
XX SQ Sequence 444 AA;
Query Match 2.4%; Score 13; DB 23; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 LHCTRNHYHMLF 184
Db 157 LHCTRNHYHMLF 169
RESULT 49
ABB56393
ID ABB56393 standard; Protein; 457 AA.
XX AC ABB56393;
XX DT 18-FEB-2002 (first entry)
XX DE Non-endogenous human GPCR protein, SEQ ID NO: 579.
XX KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; agonist; disease.

```
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200177172-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 05-APR-2001; 2001WO-US11098.
XX XX
XX PR 07-APR-2000; 2000US-195747P.
XX XX
XX PA (AREN-) ARENA PHARM INC.
XX PI Lehmann-Bruinsma K, Liaw CW, Lin I;
XX XX
XX DR WPI; 2001-648759/74.
XX DR N-PSDB; ABI98029.
XX XX
XX PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
XX PT disease treatment, comprises contacting candidate compounds with
XX PT versions of GPCRs -
XX XX
XX PS Claim 1; Page 381-383; 394pp; English.
XX XX
XX CC The invention relates to G protein-coupled receptors (GPCRs) for which
XX CC the endogenous ligand has been identified. Non-endogenous
XX CC constitutively activated versions of known GPCRs are used in the
XX CC invention for the direct identification of candidate compounds as
XX CC receptor agonists, inverse agonists or partial agonists. Such
XX CC agonists are useful as therapeutic agents for diseases or disorders
XX CC associated with GPCRs. The present sequence is a non-endogenous
XX CC version of a known human GPCR.
XX XX
XX SQ Sequence 457 AA;

Query Match 2.4%; Score 13; DB 22; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
DB 170 LHCTRNVIHMLF 182
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RESULT 50
AAB71878
ID AAB71878 standard; Protein; 457 AA.
XX
XX AC AAB71878;
XX
XX DT 03-MAY-2001 (first entry)
XX
XX DE Human VIPR seven transmembrane domain.
XX
XX KW Human; h15571; immunomodulatory; vascular; hepatic; antiasthma; VIPR;
XX KW pituitary adenylate cyclase activating polypeptide type II receptor;
XX KW antimicrobial; antiinflammatory; immunosuppressive; gene therapy;
XX KW vaccine; G-protein coupled receptor; GPCR; liver fibrosis;
XX KW respiratory disorder; infection; chronic inflammatory disease;
XX KW organ-specific autoimmunity; graft rejection; cystic fibrosis.
XX
XX OS Homo sapiens.
XX XX
XX PN WO200109328-A1.
XX XX
XX PD 08-FEB-2001.
XX XX
XX PF 03-AUG-2000; 2000WO-US21278.
XX XX
XX PR 03-AUG-1999; 99US-0146916.
XX PR 29-FEB-2000; 2000US-0515781.
```

```
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Hodge MR, Lloyd C, Weich NS;
XX
XX DR WPI; 2001-138653/14.
XX
XX PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
XX PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
XX PT -
XX
XX PS Disclosure; Fig 2; 145pp; English.
XX
XX CC The present sequence is a human G-protein coupled receptor (GPCR) used
XX CC for comparison with the seven transmembrane domain of a novel GPCR
XX CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
XX CC used in the prevention, treatment and diagnosis of diseases associated
XX CC with inappropriate GPCR expression. Such diseases includes immune,
XX CC haematological, fibrotic, hepatic and respiratory disorders including
XX CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
XX CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
XX CC graft rejection, liver fibrosis. The GPCR polypeptides may be used as antigens
XX CC in the production of antibodies against GPCR and in assays to identify
XX CC modulators (agonists and antagonists) of GPCR expression and activity.
XX CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
XX CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
XX CC used as diagnostic agents for detecting the presence of GPCR
XX CC polypeptides in samples.
XX
XX SQ Sequence 457 AA;
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Query Match 2.4%; Score 13; DB 22; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 172 LHCTRNVIHMLF 184
DB 170 LHCTRNVIHMLF 182
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Search completed: December 9, 2003, 09:00:43
Job time : 49 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2003, 08:59:50 ; Search time 21 Seconds
(without alignments)
1090.008 Million cell updates/sec

Title: US-09-996-569-2
Perfect score: 541
Sequence: 1 MAWLGLASLHWGMLGSL.....DDLMEKPSRPMESNPDTEG 541

Scoring table: OLIGO
Gapex 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	541	3	US-08-468-011A-2
2	541	100.0	541	4	US-09-236-468A-2
3	541	100.0	541	5	US-09-236-468A-2
4	60	11.1	60	3	US-08-468-011A-9
5	60	11.1	60	3	US-08-468-011A-11
6	60	11.1	60	3	US-08-468-011A-15
7	60	11.1	60	3	US-08-468-011A-19
8	60	11.1	60	4	US-09-236-468A-9
9	60	11.1	60	4	US-09-236-468A-11
10	60	11.1	60	4	US-09-236-468A-15
11	60	11.1	60	4	US-09-236-468A-19
12	59	10.9	59	3	US-08-468-011A-23
13	59	10.9	59	4	US-09-236-468A-23
14	52	9.6	52	4	US-09-236-468A-13
15	37	6.8	37	3	US-08-468-011A-25
16	37	6.8	37	4	US-09-236-468A-25
17	37	6.8	37	5	US-08-468-011A-13
18	27	5.0	27	5	US-09-449-632-5
19	25	4.6	60	3	US-08-468-011A-20
20	25	4.6	60	4	US-09-236-468A-20
21	25	4.6	515	2	US-08-468-249A-18
22	25	4.6	585	1	US-08-142-439A-6
23	25	4.6	585	2	US-08-142-551B-125
24	25	4.6	585	2	US-08-869-477-6
25	25	4.6	585	2	US-08-468-249A-19
26	21	3.9	21	3	US-08-468-011A-21
27	21	3.9	21	4	US-09-236-468A-21

28	19	3.5	449	1	US-08-142-439A-5	Sequence 5, Appli
29	19	3.5	449	2	US-08-869-477-5	Sequence 2, Appli
30	18	3.3	536	4	US-09-449-632-2	Sequence 2, Appli
31	18	3.3	591	2	US-08-468-249A-20	Sequence 20, Appl
32	18	3.3	591	2	US-08-468-249A-21	Sequence 21, Appl
33	14	2.6	19	1	US-07-864-475A-7	Sequence 7, Appli
34	14	2.6	19	2	US-08-468-249A-7	Sequence 7, Appli
35	14	2.6	60	3	US-08-468-011A-10	Sequence 10, Appl
36	14	2.6	60	4	US-09-236-468A-10	Sequence 10, Appl
37	13	2.4	458	1	US-08-112-817C-2	Sequence 2, Appli
38	13	2.4	1324	2	US-08-811-897A-56	Sequence 2, Appli
39	13	2.4	1324	4	US-09-201-474-56	Sequence 56, Appl
40	12	2.2	445	4	US-09-414-189-1	Sequence 56, Appl
41	11	2.0	542	4	US-09-449-632-4	Sequence 4, Appli
42	10	1.8	10	3	US-08-468-011A-17	Sequence 17, Appl
43	10	1.8	10	4	US-09-236-468A-17	Sequence 17, Appl
44	10	1.8	162	1	US-08-453-956-18	Sequence 18, Appl
45	10	1.8	162	1	US-08-086-631-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-468-011A-2
; Sequence 2, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLD74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-2

Query Match 100.0%; Score 541; DB 3; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLASLHWGMLGSLARQLDSGTTTIEQIVLVKAKVQCELMITAQLQEGE 60
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Db 1 MAMLGASLHVWGLMGLSCCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITAQLQEGE 60
QY 61 GNCPEPDGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKNTWA 120
Db 61 GNCPEPDGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKNTWA 120
QY 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYISFGSLAVAILIIGYFRRLHCTRNYYIH 180
Db 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYISFGSLAVAILIIGYFRRLHCTRNYYIH 180
QY 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
Db 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
QY 241 VMIYIYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAAFVAAWAVARAT 300
Db 241 VMIYIYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAAFVAAWAVARAT 300
QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFPLNTVRVLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWYQAPILAAIGLNFILFPLNTVRVLATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFQGFVFSIIYCYCNGEV 420
Db 361 LAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFQGFVFSIIYCYCNGEV 420
QY 421 QAEVKQWNRWNLVSDWKRTPPCGSRRCGSLVTTVTHSTSSQSQVAAAHAHAWCLSLAKLPR 480
Db 421 QAEVKQWNRWNLVSDWKRTPPCGSRRCGSLVTTVTHSTSSQSQVAAAHAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAMSQVTSQRTASHTLSTRSNKEDSGRORDDILMEKSRPMESNPDTTE 540
Db 481 SPADSLTATSLYLAMSQVTSQRTASHTLSTRSNKEDSGRORDDILMEKSRPMESNPDTTE 540
QY 541 G 541
Db 541 G 541

RESULT 2
US-09-236-468A-2
; Sequence 2, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 2
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-2

Query Match 100.0%; Score 541; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMLGASLHVWGLMGLSCCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITAQLQEGE 60
Db 1 MAMLGASLHVWGLMGLSCCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITAQLQEGE 60
QY 61 GNCPEPDGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKNTWA 120
Db 61 GNCPEPDGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKNTWA 120
QY 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYISFGSLAVAILIIGYFRRLHCTRNYYIH 180
Db 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYISFGSLAVAILIIGYFRRLHCTRNYYIH 180
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Db 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYISFGSLAVAILIIGYFRRLHCTRNYYIH 180
QY 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
Db 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
QY 241 VMIYIYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAAFVAAWAVARAT 300
Db 241 VMIYIYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAAFVAAWAVARAT 300
QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFPLNTVRVLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWYQAPILAAIGLNFILFPLNTVRVLATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFQGFVFSIIYCYCNGEV 420
Db 361 LAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFQGFVFSIIYCYCNGEV 420
QY 421 QAEVKQWNRWNLVSDWKRTPPCGSRRCGSLVTTVTHSTSSQSQVAAAHAHAWCLSLAKLPR 480
Db 421 QAEVKQWNRWNLVSDWKRTPPCGSRRCGSLVTTVTHSTSSQSQVAAAHAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAMSQVTSQRTASHTLSTRSNKEDSGRORDDILMEKSRPMESNPDTTE 540
Db 481 SPADSLTATSLYLAMSQVTSQRTASHTLSTRSNKEDSGRORDDILMEKSRPMESNPDTTE 540
QY 541 G 541
Db 541 G 541

RESULT 3
PCT-US95-07085-2
; Sequence 2, Application PC/TUS9507085
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07085
; FILING DATE: 05-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-393
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07085-2
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Query Match 100.0%; Score 541; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAWLGLSLHVGWMLGSCLLARAQLDSQDTTIEQIVLVKAKVQCELNITAOIQE 60

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DB 61 GNCFFPNDGLICWPRGTGKISAVPCPPYIYDNNKGVAFRHCNPNGTWDFMHSLNK 120

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DB 121 NTSDCLEFLQPDISIGKQFCERLYVMYTVGVISFGSLAVAILIIGYFRRLHCT 180

QY 181 MHLFVSEMLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVKSOVIGCKIAV 240
DB 181 MHLFVSEMLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVKSOVIGCKIAV 240

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DB 241 VMFIYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILIGWGPAAFAVAW 300

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DB 301 LADARWELSGDIKIWIYQAPILAAIGLNFILFNTVRVLATKINETNAVGHDT 360

QY 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRHCELFNSFQGFVSIYCYNGEV 420
DB 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRHCELFNSFQGFVSIYCYNGEV 420

QY 421 QAEVKKMSRWNLVDVKKTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCLSLAK 480
DB 421 QAEVKKMSRWNLVDVKKTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCLSLAK 480

QY 481 SPADSLTATSLYAMSGVTOSTASHTLSTRNKEDSGRQDDILMEKPSRMESNP 540
DB 481 SPADSLTATSLYAMSGVTOSTASHTLSTRNKEDSGRQDDILMEKPSRMESNP 540

QY 541 G 541
DB 541 G 541

RESULT 4
US-08-468-011A-9
; Sequence 9, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-11

FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-011A-9

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 IMQDDPQNSIEATSVKSOYIGCKIAVVMFIYFLATNYWILVEGLYLNHLIFVAF 273
DB 1 IMQDDPQNSIEATSVKSOYIGCKIAVVMFIYFLATNYWILVEGLYLNHLIFVAF 60

RESULT 5
US-08-468-011A-11
; Sequence 11, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-11

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 KYLWGFILGWGFPAAFAVAVARATLADARCWELSGAGDIKWTYQAPILAAIGLNTLF 333
Db 1 KYLWGFILGWGFPAAFAVAVARATLADARCWELSGAGDIKWTYQAPILAAIGLNTLF 60

RESULT 6

US-08-468-011A-15
; Sequence 15, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-15

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 60 EGNCFPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTW 119
Db 1 EGNCFPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTW 60

RESULT 7

US-08-468-011A-19
; Sequence 19, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,

; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-19

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 137 KQFECRLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNYYIMHLFVSPMLRATSIYV 196
Db 1 KQFECRLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNYYIMHLFVSPMLRATSIYV 60

RESULT 8

US-09-236-468A-9
; Sequence 9, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-9

Query Match 11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 214 IMODDPQNSIATSVDKSOYIGCKIAVVMFIYFLATNYYWILVEGLYHNLIFVAFPSDT 273
Db 1 IMODDPQNSIATSVDKSOYIGCKIAVVMFIYFLATNYYWILVEGLYHNLIFVAFPSDT 60

RESULT 9

US-09-236-468A-11
; Sequence 11, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:

APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-11

Query Match 11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 KYLWGHILGWGFPFAAFAVAARATLADARCWELSGADIKWIYQAPILAAIGLNFILF 333
DB 1 KYLWGFILGWGFPFAAFAVAARATLADARCWELSGADIKWIYQAPILAAIGLNFILF 60

RESULT 10
US-09-236-468A-15
; Sequence 15, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-15

Query Match 11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 EGNCFPEWDGLICWRGTGKISAVPCPPYIYDFNHKGVAFRCNPNGTWDPMHSLNKTW 119
DB 1 EGNCFPEWDGLICWRGTGKISAVPCPPYIYDFNHKGVAFRCNPNGTWDPMHSLNKTW 60

RESULT 11
US-09-236-468A-19
; Sequence 19, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-19

Query Match 11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 KOEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTHMILFVSMRLRATSIYV 196
DB 1 KOEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTHMILFVSMRLRATSIYV 60

RESULT 12
US-08-468-011A-23
; Sequence 23, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-23

Query Match 10.9%; Score 59; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.6e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 TGLGWEIRMHCELFNSFGSFVSIYCYCNGEYQAEVKQKWSRWLSVDWKRTPPCGS 445
DB 1 TGLGWEIRMHCELFNSFGSFVSIYCYCNGEYQAEVKQKWSRWLSVDWKRTPPCGS 59

RESULT 13
US-09-236-468A-23
; Sequence 23, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011

; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-23

Query Match 10.9%; Score 59; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.6e-48; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 387 TGLGWEIRHCELFNFQGFVSIYYCNGEYQAEVKWGRNLSVDWKRTPPCGS 445
Db 1 TGLGWEIRHCELFNFQGFVSIYYCNGEYQAEVKWGRNLSVDWKRTPPCGS 59

RESULT 14
US-09-236-468A-13
; Sequence 13, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-13

Query Match 9.6%; Score 52; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3e-41; Indels 0; Gaps 0;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 LNTVRVLATKIWETNAVGHDTKQYRKLAKSTLVLVFGVHYIVFVCLPHS 385
Db 1 LNTVRVLATKIWETNAVGHDTKQYRKLAKSTLVLVFGVHYIVFVCLPHS 52

RESULT 15
US-08-468-011A-25
; Sequence 25, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-25

Query Match 6.8%; Score 37; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-27; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 AQLSDGTTTIEQIVLVLKAKVQCELNITAIQLQEGE 60
Db 1 AQLSDGTTTIEQIVLVLKAKVQCELNITAIQLQEGE 37

RESULT 16
US-09-236-468A-25
; Sequence 25, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-25

Query Match 6.8%; Score 37; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-27; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 AQLSDGTTTIEQIVLVLKAKVQCELNITAIQLQEGE 60
Db 1 AQLSDGTTTIEQIVLVLKAKVQCELNITAIQLQEGE 37

RESULT 17
US-08-468-011A-13
; Sequence 13, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland

```

; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; OPERATING SYSTEM: IBM PS/2
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-13

Query Match          6.8%; Score 37; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.7e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 LNTVRVLAKIWTNAVGHDTKQYRKLAKSLVLVL 370
DB 1 LNTVRVLAKIWTNAVGHDTKQYRKLAKSLVLVL 37

RESULT 18
US-09-449-632-5
; Sequence 5, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Ruben, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 50/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: zebrafish
US-09-449-632-5

Query Match          5.0%; Score 27; DB 4; Length 575;
Best Local Similarity 100.0%; Pred. No. 4.2e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 IIGYFRLHCTRNVIHMHFLVFSFMLRA 191
DB 193 IIGYFRLHCTRNVIHMHFLVFSFMLRA 219

RESULT 19
US-08-468-011A-20
; Sequence 20, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li

```

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; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-20

Query Match          4.6%; Score 25; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNVIHMHFLVFSFMLRA 191
DB 31 GYFRLHCTRNVIHMHFLVFSFMLRA 55

RESULT 20
US-09-236-468A-20
; Sequence 20, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Didelphis virginiana
US-09-236-468A-20

Query Match          4.6%; Score 25; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNVIHMHFLVFSFMLRA 191
DB 31 GYFRLHCTRNVIHMHFLVFSFMLRA 55

```

RESULT 21
US-08-468-249A-18
; Sequence 18, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-18
Query Match 4.6%; Score 25; DB 2; Length 515;
Best Local Similarity 100.0%; Pred. No. 2.9e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 167 GYFRRLHCTRNTHMLFVSFMLRA 191
Db 207 GYFRRLHCTRNTHMLFVSFMLRA 231
RESULT 22
US-08-142-439A-6
; Sequence 6, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56703600 No. 56703600disk of No. 56703600th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
US-08-142-439A-6
Query Match 4.6%; Score 25; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 167 GYFRRLHCTRNTHMLFVSFMLRA 191
Db 207 GYFRRLHCTRNTHMLFVSFMLRA 231
RESULT 23
US-08-142-551B-125
; Sequence 125, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oidenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993

;; PRIOR APPLICATION DATA: US 07/898,219
;; FILING DATE: 12-JUN-1992
;; APPLICATION NUMBER: US 07/965,677
;; FILING DATE: 22-OCT-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Swiss, Gerald F.
;; REGISTRATION NUMBER: 30,113
;; REFERENCE/DOCKET NUMBER: 000324-010
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 854-7400
;; TELEFAX: (415) 854-8275
;; INFORMATION FOR SEQ ID NO: 125:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 585 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..585
;; OTHER INFORMATION: /note= "PTH receptor"
;; US-08-142-551B-125

Query Match 4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRYIHMLFVSFMLRA 191
|||||
Db 207 GYFRRLHCTRYIHMLFVSFMLRA 231

RESULT 24

US-08-869-477-6
; Sequence 6, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123

;; TELEFAX: 212 867 0298
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 585 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Didelphis virginiana
;; US-08-869-477-6

Query Match 4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRYIHMLFVSFMLRA 191
|||||
Db 207 GYFRRLHCTRYIHMLFVSFMLRA 231

RESULT 25

US-08-468-249A-19
; Sequence 19, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al.; Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-249A-19

Query Match 4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRYIHMLFVSFMLRA 191
Db 207 GYFRLHCTRYIHMLFVSFMLRA 231

RESULT 26

US-08-468-011A-21
; Sequence 21, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTGD74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Oistein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J. G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-21

Query Match 3.9%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 KDRVVAHIGVKELESIMQD 217
Db 1 KDRVVAHIGVKELESIMQD 21

RESULT 27

US-09-236-468A-21
; Sequence 21, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTGD74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21

; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-21

Query Match 3.9%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.8e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 KDRVVAHIGVKELESIMQD 217
Db 1 KDRVVAHIGVKELESIMQD 21

RESULT 28

US-08-142-439A-5
; Sequence 5, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5670360o No. 5670360disk of No. 5670360th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; STRANDEDNESS: single
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
US-08-142-439A-5

Query Match 3.5%; Score 19; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRELHCTRYIHMLFVSF 187
Db 167 FRELHCTRYIHMLFVSF 185

RESULT 29
US-08-869-477-5
; Sequence 5, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; STREET: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
US-08-869-477-5

Query Match 3.5%; Score 19; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLLHCTRYNIHMLFVVSF 187
|||||
DB 167 FRRLLHCTRYNIHMLFVVSF 185

RESULT 30
US-09-449-632-2
; Sequence 2, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHR1R and PTHR3R Receptors, Methods and Uses Thereof

; FILE REFERENCE: 0609,4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: zebrafish
US-09-449-632-2

Query Match 3.3%; Score 18; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLLHCTRYNIHMLF 184
|||||
DB 167 GYFRRLLHCTRYNIHMLF 184

RESULT 31
US-08-468-249A-20
; Sequence 20, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-20

Query Match 3.3%; Score 18; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYTWILVEGLYLH 262

Db 290 YFLATNYWILVEGLYH 307
|||||

RESULT 32
US-08-468-249A-21
; Sequence 21, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-21

Query Match 3.3%; Score 18; DB 2; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262
Db 290 YFLATNYWILVEGLYH 307
|||||

RESULT 33
US-07-864-475A-7
; Sequence 7, Application US/07864475A
; Patent No. 5494806
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T. [Jr.]
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864,475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-07-864-475A-7
Query Match 2.6%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEG 258
Db 6 YFLATNYWILVEG 19
|||||

RESULT 34
US-08-468-249A-7
; Sequence 7, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-249A-7

Query Match 2.6%; Score 14; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEG 258
DB 6 YFLATNYWILVEG 19

RESULT 35
US-08-468-011A-10
Sequence 10, Application US/08468011A
Patent No. 6030804
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven
APPLICANT: Rosen, Craig A
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
TITLE OF INVENTION: HLTDG74
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-011A-10

Query Match 2.6%; Score 14; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 249 TNYWILVEGLYLH 262
DB 36 TNYWILVEGLYLH 49

RESULT 36
US-09-236-468A-10
Sequence 10, Application US/09236468A
Patent No. 6338951
GENERAL INFORMATION:
APPLICANT: Soppet et al.
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
FILE REFERENCE: PF201D1
CURRENT APPLICATION NUMBER: US/09/236,468A
CURRENT FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 08/468,011
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 10
LENGTH: 60
TYPE: PRT
ORGANISM: Didelphis virginiana
US-09-236-468A-10

Query Match 2.6%; Score 14; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 TNYWILVEGLYLH 262
DB 36 TNYWILVEGLYLH 49

RESULT 37
US-08-112-817C-2
Sequence 2, Application US/08112817C
Patent No. 5573928
GENERAL INFORMATION:
APPLICANT: Hsiung, Hansen M.
APPLICANT: Smith, Dennis P.
APPLICANT: Zhang, Xing-Yue
TITLE OF INVENTION: PORCINE VASOACTIVE INTESTINAL PEPTIDE
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh IIfx compatible
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word for Macintosh v.5.1a
CURRENT APPLICATION DATA:
FILING DATE: US/08/112.817C
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Richard B.
REGISTRATION NUMBER: 35,296
REFERENCE/DOCKET NUMBER: X-9293
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3589
TELEFAX: 317-276-1294
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-112-817C-2

Query Match 2.4%; Score 13; DB 1; Length 458;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRYNIHMLF 184
|||||
Db 171 LHCTRYNIHMLF 183

RESULT 38

US-08-811-897A-56
; Sequence 56, Application US/08811897A
; Patent No. 5858787

GENERAL INFORMATION:

; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSOYA, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 5858787io
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811.897A
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: February 25, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1324 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-811-897A-56

Query Match 2.4%; Score 13; DB 2; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRYNIHMLF 184
|||||
Db 171 LHCTRYNIHMLF 183

RESULT 39

US-09-201-474-56
; Sequence 56, Application US/09201474
; Patent No. 6399316
; GENERAL INFORMATION:

; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSOYA, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 6399316io
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,897
; FILING DATE: 05-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1324 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-201-474-56

Query Match 2.4%; Score 13; DB 4; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRYNIHMLF 184
|||||
Db 173 LHCTRYNIHMLF 185

RESULT 40

US-09-414-189-1
; Sequence 1, Application US/09414189
; Patent No. 6410508
; GENERAL INFORMATION:

; APPLICANT: Isales, Carlos M.
; APPLICANT: Bollag, Roni J.
; APPLICANT: Rasmussen, Howard

```
; TITLE OF INVENTION: Glucose-dependent Insulinotropic Peptide for Use as an
; FILE REFERENCE: MCG 108
; CURRENT APPLICATION NUMBER: US/09/414,189
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: From 6-25 synthetic oligopeptide region used to
; make antibodies blocking GIP receptor activation
US-09-414-189-1

Query Match      2.2%; Score 12; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIH 180
Db 141 FRLHCTRNVIH 152

RESULT 41
US-09-449-632-4
; Sequence 4, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: zebrafish
US-09-449-632-4

Query Match      2.0%; Score 11; DB 4; Length 542;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 YWILVEGLYH 262
Db 236 YWILVEGLYH 246

RESULT 42
US-08-468-011A-17
; Sequence 17, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; FILE REFERENCE: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
```

```
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PP201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-17

Query Match      1.8%; Score 10; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ANYSDCLRFL 129
Db 1 ANYSDCLRFL 10

RESULT 43
US-09-236-468A-17
; Sequence 17, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-17

Query Match      1.8%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ANYSDCLRFL 129
Db 1 ANYSDCLRFL 10

RESULT 44
US-08-453-956-18
; Sequence 18, Application US/08453956
; Patent No. 5770445
; GENERAL INFORMATION:
; APPLICANT: Kindvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
```

; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 99104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,956
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELEPHONE: 206-622-4900
; TELEFAX: 206-622-6031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-453-956-18

Query Match 1.8%; Score 10; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYLHNL 264
| | | | | | | | | |
Db 99 LVEGLYLHNL 108

RESULT 45
US-08-086-631-18
; Sequence 18, Application US/08086631
; Patent No. 5776725
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 99104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,631
; FILING DATE: July 1, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.

; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-086-631-18

Query Match 1.8%; Score 10; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYLHNL 264
| | | | | | | | | |
Db 99 LVEGLYLHNL 108

RESULT 46
US-08-452-930-18
; Sequence 18, Application US/08452930
; Patent No. 5919635
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 99104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,930
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-452-930-18

Query Match 1.8%; Score 10; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYLHNL 264
| | | | | | | | | |
Db 99 LVEGLYLHNL 108

```
RESULT 47
PCT-US93-08174-18
; Sequence 18, Application PC/TUS9308174
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: NAME: ZymoGenetics, Inc.
; APPLICANT: STREET: 4225 Roosevelt Way North East
; APPLICANT: CITY: Seattle, Washington
; APPLICANT: COUNTRY: United States
; APPLICANT: POSTAL CODE: 98105
; APPLICANT: TELEPHONE: (206) 547-80808
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08174
; FILING DATE: 30-AUG-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMaisters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-08174-18

Query Match 1.8%; Score 10; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYHLNL 264
Db 99 LVEGLYHLNL 108

RESULT 48
US-08-845-546-10
; Sequence 10, Application US/08845546
; Patent No. 6077949
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald
; APPLICANT: Gupta, Ashwani
; APPLICANT: Vyas, Tejal
; APPLICANT: McCallum, Kirk
; APPLICANT: Fan, Ermei
; TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE
; NUMBER OF SEQUENCES: 24
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,546
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8607-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-845-546-10

Query Match 1.8%; Score 10; DB 3; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNVIHM 181
Db 20 LHCTRNVIHM 29

RESULT 49
US-08-453-956-25
; Sequence 25, Application US/08453956
; Patent No. 5770445
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,956
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMaisters, David D.
```

Search completed: December 9, 2003, 09:03:13
Job time : 23 secs

REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008.424C1
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-956-25

Query Match 1.8%; Score 10; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
Db 243 LVEGLYLHNL 252

RESULT 50

US-08-086-631-25
Sequence 25, Application US/08086631
Patent No. 5776725
GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne R.
TITLE OF INVENTION: GLUCAGON RECEPTORS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 COLUMBIA CENTER
CITY: SEATTLE
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,631
FILING DATE: July 1, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008.424C1
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-086-631-25

Query Match 1.8%; Score 10; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
Db 243 LVEGLYLHNL 252

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2003, 09:02:11 ; Search time 37 Seconds
(without alignments)

2719.383 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGLASLHWGMLGSL.....DDILMEKSPHESNPDTEG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 684280 seqs, 185983659 residues

Word size : 0

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	363	67.1	550	15	US-10-225-567A-227
2	262	48.4	550	12	US-09-826-509-565
3	216	39.9	550	15	US-10-014-162-110
4	33	6.1	546	15	US-10-014-162-109
5	27	5.0	575	12	US-10-372-095-5
6	25	4.6	515	12	US-10-267-730-18
7	25	4.6	585	12	US-10-267-730-19
8	20	3.7	20	15	US-10-225-567A-1225
9	19	3.5	353	12	US-10-017-161-696
10	19	3.5	440	12	US-09-826-509-567
11	19	3.5	440	15	US-10-225-567A-310
12	18	3.3	18	15	US-10-225-567A-1224
13	18	3.3	536	12	US-10-372-095-2
14	18	3.3	591	10	US-09-943-446-7
15	18	3.3	591	10	US-09-943-446-8

16	18	3.3	591	12	US-10-267-730-20
17	18	3.3	593	10	US-09-943-446-9
18	18	3.3	593	12	US-10-267-730-21
19	18	3.3	593	12	US-09-826-509-563
20	18	3.3	593	15	US-10-225-567A-229
21	18	3.3	595	10	US-09-943-446-6
22	18	3.3	964	12	US-10-017-161-710
23	14	2.6	19	12	US-10-267-730-7
24	13	2.4	457	12	US-09-826-509-579
25	13	2.4	457	15	US-10-225-567A-469
26	13	2.4	1324	10	US-09-935-371-56
27	12	2.2	268	9	US-09-796-338A-19
28	12	2.2	268	12	US-10-145-586-19
29	12	2.2	268	12	US-10-407-079-95
30	12	2.2	268	15	US-10-282-837-19
31	12	2.2	271	9	US-09-795-693-36
32	12	2.2	271	15	US-10-156-239-36
33	12	2.2	271	15	US-10-199-485-36
34	12	2.2	466	12	US-10-241-220-78
35	12	2.2	466	12	US-09-826-509-507
36	12	2.2	466	15	US-10-225-567A-128
37	11	2.0	542	12	US-10-372-095-4
38	10	1.8	11	10	US-09-966-871-62
39	10	1.8	11	14	US-10-039-645-62
40	10	1.8	11	15	US-10-139-084-62
41	10	1.8	273	15	US-10-120-604-11
42	10	1.8	477	14	US-10-010-065-6
43	10	1.8	477	15	US-10-225-567A-134
44	10	1.8	553	15	US-10-225-567A-520
45	9	1.7	10	10	US-09-966-871-67

ALIGNMENTS

RESULT 1

US-10-225-567A-227
; Sequence 227, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-227

Query Match 67.1%; Score 363; DB 15; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	4	LGASLHWGMLGSLARQLDSGGTITTEEQIVLVKAKVQCELNITAQLEGHCNC 63
DB	4	LGASLHWGMLGSLARQLDSGGTITTEEQIVLVKAKVQCELNITAQLEGHCNC 63
QY	64	FPFWDGLICWPRGVGKISAVPCPPYIDFNHKGVAFCNPNGTWDFHSLINKTWANYS 123
DB	64	FPFWDGLICWPRGVGKISAVPCPPYIDFNHKGVAFCNPNGTWDFHSLINKTWANYS 123
QY	124	DCLRFLOPDISIGKQEFCELYVMYTVGYSISFGSLAVAILIIGYFRHLHCTRYIHML 183
DB	124	DCLRFLOPDISIGKQEFCELYVMYTVGYSISFGSLAVAILIIGYFRHLHCTRYIHML 183

QY 184 FVSFMLRATSI FVKDRVVAHIGVKELESIMODDPQNSIEATSVKDSQYIGCKIAVWF 243
DB 184 FVSFMLRATSI FVKDRVVAHIGVKELESIMODDPQNSIEATSVKDSQYIGCKIAVWF 243
QY 244 IYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFIICGWGPPAFAVAWAVARATLAD 303
DB 244 IYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFIICGWGPPAFAVAWAVARATLAD 303
QY 304 ARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLTATKIWETNAVGHDTKQYRKLAK 363
DB 304 ARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLTATKIWETNAVGHDTKQYRKLAK 363
QY 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCCLFFNSFOGFFVSIICYCNGEVOAE 423
DB 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCCLFFNSFOGFFVSIICYCNGEVOAE 423
QY 424 VKOWSRNLSVDWKRTPPCGSRRCGSLVLTTHSTSSQSOVAA 467
DB 424 VKOWSRNLSVDWKRTPPCGSRRCGSLVLTTHSTSSQSOVAA 467
RESULT 2
US-09-826-509-565
; Sequence 565, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-tin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 565
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-565

Query Match 48.4%; Score 262; DB 12; Length 550;
Best Local Similarity 99.8%; Pred. No. 5.4e-250;
Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 LGASLHVWGLMGLSCLLARAQLDSGTITIEBQIVLVLKAKVQCEBLNITAOQEGGNC 63
DB 4 LGASLHVWGLMGLSCLLARAQLDSGTITIEBQIVLVLKAKVQCEBLNITAOQEGGNC 63
QY 64 FPEWDLICMPRTGVKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 123
DB 64 FPEWDLICMPRTGVKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 123
QY 124 DCLRFLOPDISGQFCERLYWYTVGYSISFGSLAVAILIIGYPRRLHCTRNHYHML 183
DB 124 DCLRFLOPDISGQFCERLYWYTVGYSISFGSLAVAILIIGYPRRLHCTRNHYHML 183
QY 184 FVSFMLRATSI FVKDRVVAHIGVKELESIMODDPQNSIEATSVKDSQYIGCKIAVWF 243
DB 184 FVSFMLRATSI FVKDRVVAHIGVKELESIMODDPQNSIEATSVKDSQYIGCKIAVWF 243
QY 244 IYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFIICGWGPPAFAVAWAVARATLAD 303
DB 244 IYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFIICGWGPPAFAVAWAVARATLAD 303
QY 304 ARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLTATKIWETNAVGHDTKQYRKLAK 363

DB 304 ARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLTATKIWETNAVGHDTKQYRKLAK 363
QY 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCCLFFNSFOGFFVSIICYCNGEVOAE 423
DB 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCCLFFNSFOGFFVSIICYCNGEVOAE 423
QY 424 VKOWSRNLSVDWKRTPPCGSRRCGSLVLTTHSTSSQSOVAA 467
DB 424 VKOWSRNLSVDWKRTPPCGSRRCGSLVLTTHSTSSQSOVAA 467

RESULT 3

US-10-014-162-110
; Sequence 110, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-162-110

Query Match 39.9%; Score 216; DB 15; Length 550;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 YWILVEGLYHNLIFVAFPSDTKYLWGFIICGWGPPAFAVAWAVARATLADARCWELSA 311
DB 252 YWILVEGLYHNLIFVAFPSDTKYLWGFIICGWGPPAFAVAWAVARATLADARCWELSA 311
QY 312 GDKWIYQAPILAAIGLNFILNTVRVLTATKIWETNAVGHDTKQYRKLAKSTLVVLV 371
DB 312 GDKWIYQAPILAAIGLNFILNTVRVLTATKIWETNAVGHDTKQYRKLAKSTLVVLV 371
QY 372 FGWHIVFVCLPHSFTGLGWEIRHMCCLFFNSFOGFFVSIICYCNGEVOAEVKOWSRW 431
DB 372 FGWHIVFVCLPHSFTGLGWEIRHMCCLFFNSFOGFFVSIICYCNGEVOAEVKOWSRW 431
QY 432 NLSVDWKRTPPCGSRRCGSLVLTTHSTSSQSOVAA 467
DB 432 NLSVDWKRTPPCGSRRCGSLVLTTHSTSSQSOVAA 467

RESULT 4

US-10-014-162-109
; Sequence 109, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109

LENGTH: 546
TYPE: PRT
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(546)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-014-162-109

Query Match 6.1%; Score 33; DB 15; Length 546;
Best Local Similarity 100.0%; Pred. No. 9.3e-24;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YTVGISISFGSLAVAILIIGYFRLHCTRNTH 180
DB 146 YTVGISISFGSLAVAILIIGYFRLHCTRNTH 178

RESULT 5

US-10-372-095-5
Sequence 5, Application US/10372095
Publication No. US20030162256A1
GENERAL INFORMATION:
APPLICANT: Juppner, Harald
APPLICANT: Rubin, David A.
TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
FILE REFERENCE: 0609 4740002
CURRENT APPLICATION NUMBER: US/10/372,095
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/449,632
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: US 60/110,467
PRIOR FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 5
LENGTH: 575
TYPE: PRT
ORGANISM: Danio rerio
US-10-372-095-5

Query Match 5.0%; Score 27; DB 12; Length 575;
Best Local Similarity 100.0%; Pred. No. 8.3e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 IIGYFRLHCTRNTHMHLFVSFMLRA 191
DB 193 IIGYFRLHCTRNTHMHLFVSFMLRA 219

RESULT 6

US-10-267-730-18
Sequence 18, Application US/10267730
Publication No. US20030153041A1
GENERAL INFORMATION:
APPLICANT: Segre, Gino V.
APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Potts, Jr., John T.
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
FILE REFERENCE: 00786/071005
CURRENT APPLICATION NUMBER: US/10/267,730
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 08/471,494
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 515
TYPE: PRT
ORGANISM: Didelphoidea

US-10-267-730-18

Query Match 4.6%; Score 25; DB 12; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.1e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNTHMHLFVSFMLRA 191
DB 207 GYFRLHCTRNTHMHLFVSFMLRA 231

RESULT 7

US-10-267-730-19
Sequence 19, Application US/10267730
Publication No. US20030153041A1
GENERAL INFORMATION:
APPLICANT: Segre, Gino V.
APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Potts, Jr., John T.
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
FILE REFERENCE: 00786/071005
CURRENT APPLICATION NUMBER: US/10/267,730
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 08/471,494
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 585
TYPE: PRT
ORGANISM: Didelphoidea
US-10-267-730-19

Query Match 4.6%; Score 25; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 8e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNTHMHLFVSFMLRA 191
DB 207 GYFRLHCTRNTHMHLFVSFMLRA 231

RESULT 8

US-10-225-567A-1225
Sequence 1225, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patent In version 3.1
SEQ ID NO 1225
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-1225

Query Match 3.7%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 ESLIMQDDPQNSTEATSVDK 230

Db 1 ESLIMQDDPONSIEATSVDK 20
|||||

RESULT 9

US-10-017-161-696
; Sequence 696, Application US/10017161
; Publication No. US2003014368A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ASURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 696
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-696

Query Match 3.5%; Score 19; DB 12; Length 353;
Best Local Similarity 100.0%; Pred. No. 4.3e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYNIHMLFVSF 187
Db 23 FRLHCTRYNIHMLFVSF 41
|||||

RESULT 10

US-09-826-509-567
; Sequence 567, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruntsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 567
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-567

Query Match 3.5%; Score 19; DB 12; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYNIHMLFVSF 187
Db 167 FRLHCTRYNIHMLFVSF 185
|||||

RESULT 11

US-10-225-567A-310
; Sequence 310, Application US/10225567A

; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 310
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-310

Query Match 3.5%; Score 19; DB 15; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYNIHMLFVSF 187
Db 167 FRLHCTRYNIHMLFVSF 185
|||||

RESULT 12

US-10-225-567A-1224
; Sequence 1224, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1224
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1224

Query Match 3.3%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 KAKVQCELNITAOLOEGE 60
Db 1 KAKVQCELNITAOLOEGE 18
|||||

RESULT 13

US-10-372-095-2
; Sequence 2, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.474002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632

; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-2

Query Match 3.3%; Score 18; DB 12; Length 536;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRNTHMLF 184
|||
Db 167 GYFRRLHCTRNTHMLF 184

RESULT 14
US-09-943-446-7
; Sequence 7, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus No. US20020146777A1vegicus
US-09-943-446-7

Query Match 3.3%; Score 18; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262
|||
Db 290 YFLATNYWILVEGLYH 307

RESULT 15
US-09-943-446-8
; Sequence 8, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 591

; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-943-446-8

Query Match 3.3%; Score 18; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262
|||
Db 290 YFLATNYWILVEGLYH 307

RESULT 16
US-10-267-730-20
; Sequence 20, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-267-730-20

Query Match 3.3%; Score 18; DB 12; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262
|||
Db 290 YFLATNYWILVEGLYH 307

RESULT 17
US-09-943-446-9
; Sequence 9, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-943-446-9

Query Match 3.3%; Score 18; DB 10; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
| | | | | | | | | | | | | | | | | |
Db 290 YFLATNYWILVEGLYLH 307

RESULT 18

US-10-267-730-21
; Sequence 21, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-730-21

Query Match 3.3%; Score 18; DB 12; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
| | | | | | | | | | | | | | | | | |
Db 290 YFLATNYWILVEGLYLH 307

RESULT 19

US-09-826-509-563
; Sequence 563, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: Protein-Coupled Receptors
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

Query Match 3.3%; Score 18; DB 12; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
| | | | | | | | | | | | | | | | | |
Db 290 YFLATNYWILVEGLYLH 307

RESULT 20

US-10-225-567A-229
; Sequence 229, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 229
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-229

Query Match 3.3%; Score 18; DB 15; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
| | | | | | | | | | | | | | | | | |
Db 290 YFLATNYWILVEGLYLH 307

RESULT 21

US-09-943-446-6
; Sequence 6, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGER
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Canis Familiaris
US-09-943-446-6

Query Match 3.3%; Score 18; DB 10; Length 595;
Best Local Similarity 100.0%; Pred. No. 6.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
| | | | | | | | | | | | | | | | | |
Db 289 YFLATNYWILVEGLYLH 306

RESULT 22

US-10-017-161-710
; Sequence 710, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO

APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABEURATANI, HIROFUKU
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/01017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 710
LENGTH: 964
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-161-710

Query Match 3.3%; Score 18; DB 12; Length 964;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVGLYLH 262
DB 564 YFLATNYWILVGLYLH 581

RESULT 23
US-10-267-730-7
Sequence 7, Application US/10267730
Publication No. US20030153041A1
GENERAL INFORMATION:
APPLICANT: Segre, Gino V.
APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Potts, Jr., John T.
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
FILE REFERENCE: 00786/071005
CURRENT APPLICATION NUMBER: US/10/267,730
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 08/471,494
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: binding; 1st to last; peptide fragment
US-10-267-730-7

Query Match 2.6%; Score 14; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVGL 258
DB 6 YFLATNYWILVGL 19

RESULT 24
US-09-826-509-579
Sequence 579, Application US/09826509
Publication No. US20030204073A1
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
FILE REFERENCE: AREN-207

CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
CURRENT APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 579
LENGTH: 457
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-509-579

Query Match 2.4%; Score 13; DB 12; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
DB 170 LHCTRNVIHMLF 182

RESULT 25
US-10-225-567A-469
Sequence 469, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 469
LENGTH: 457
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-469

Query Match 2.4%; Score 13; DB 15; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
DB 170 LHCTRNVIHMLF 182

RESULT 26
US-09-935-371-56
Sequence 56, Application US/09935371
Patent No. US2002015533A1
GENERAL INFORMATION:
APPLICANT: ONDA, Haruo
OHTAKI, Tetsuya
MASUDA, Yasushi
KITADA, Chieko
ISHIBASHI, Yoshihiro
HOSOYA, Masaki
OGI, Kazuhiro
MIYAMOTO, Yasunori
HABATA, Yugo
SHIMAMOTO, No. US2002015533A110
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
SAID PROTEIN, AND USE THEREOF
NUMBER OF SEQUENCES: 56

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,371
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,474
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 1324 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-935-371-56
Query Match 2.4%; Score 13; DB 10; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIHMLF 184
|||||
Db 173 LHCTRYIHMLF 185

RESULT 27
US-09-796-338A-19
; Sequence 19, Application US/09796338A
; Patent No. US20020061522A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; FILE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/09/796,338A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-796-338A-19
Query Match 2.2%; Score 12; DB 9; Length 268;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYIH 180
|||||
Db 29 FRLHCTRYIH 40

RESULT 29
US-10-407-079-95
; Sequence 95, Application US/10407079
; Publication No. US20030215860A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: 19636, 2466, 43238, 1983, 52881, 2398,
; FILE OF INVENTION: 45449, 50289, 52872 AND 26908 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0510MNIM
; CURRENT APPLICATION NUMBER: US/10/407,079
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/226,102
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,041
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 10/225,094
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,185
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 10/272,417
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/715,790
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/191,845
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 10/282,837
; PRIOR FILING DATE: 2002-10-29
```

```
Db 29 FRLHCTRYIH 40
|||||
RESULT 28
US-10-145-586-19
; Sequence 19, Application US/10145586
; Publication No. US20030138890A1
; GENERAL INFORMATION:
; APPLICANT: Alexandra Glucksmann, Maria
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Weich, Nadine
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
; FILE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; CURRENT FILING DATE: 2002-05-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-145-586-19
```

```
Query Match 2.2%; Score 12; DB 12; Length 268;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYIH 180
|||||
Db 29 FRLHCTRYIH 40
```

```
RESULT 29
US-10-407-079-95
; Sequence 95, Application US/10407079
; Publication No. US20030215860A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: 19636, 2466, 43238, 1983, 52881, 2398,
; FILE OF INVENTION: 45449, 50289, 52872 AND 26908 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0510MNIM
; CURRENT APPLICATION NUMBER: US/10/407,079
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/226,102
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,041
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 10/225,094
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,185
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 10/272,417
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/715,790
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/191,845
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 10/282,837
; PRIOR FILING DATE: 2002-10-29
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; PRIOR APPLICATION NUMBER: US 09/796,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; PRIOR FILING DATE: 2000-02-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid consensus sequence
US-10-407-079-95

Query Match          2.2%; Score 12; DB 12; Length 268;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYYH 180
Db 29 FRLHCTRNYYH 40

RESULT 30
US-10-282-837-19
; Sequence 19, Application US/10282837
; Publication No. US20030082738A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/10/282,837
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/796,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-282-837-19

Query Match          2.2%; Score 12; DB 15; Length 268;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYYH 180
Db 29 FRLHCTRNYYH 40

RESULT 31
US-09-795-693-36
; Sequence 36, Application US/09795693
; Patent No. US20020068710A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
; TITLE OF INVENTION: 32613, NO. US20020068710A1 Human Transporters
; FILE REFERENCE: 35800/209292
; CURRENT APPLICATION NUMBER: US/09/795,693
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 36
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pfam consensus sequence
US-09-795-693-36

Query Match          2.2%; Score 12; DB 9; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYYH 180
Db 29 FRLHCTRNYYH 40

RESULT 32
US-10-156-239-36
; Sequence 36, Application US/10156239
; Publication No. US20030036074A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: No. US20030036074A1 Nucleic Acid Sequences Encoding Human Tr
; TITLE OF INVENTION: Atpase Molecule, A Human Ubiquitin Hydrolase-Like Molecule, A
; TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor
; FILE REFERENCE: 35800/247645
; CURRENT APPLICATION NUMBER: US/10/156,239
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/795,693
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/809,557
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/192,018
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,568
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/191,790
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,767
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/191,781
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pfam consensus sequence
US-10-156-239-36

Query Match          2.2%; Score 12; DB 15; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYYH 180
Db 29 FRLHCTRNYYH 40

RESULT 33
US-10-199-485-36
; Sequence 36, Application US/10199485
; Publication No. US20030077626A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
```

```
; TITLE OF INVENTION: 32613, No. US20030077626A1el Human Transporters
; FILE REFERENCE: 35800/249488
; CURRENT APPLICATION NUMBER: US/10/199,485
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 09/795,693
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pfam consensus sequence
US-10-199-485-36

Query Match          2.2%; Score 12; DB 15; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRHCTRNYYH 180
Db 29 FRRHCTRNYYH 40

RESULT 34
US-10-241-220-78
; Sequence 78, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 78
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-241-220-78

Query Match          2.2%; Score 12; DB 12; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRHCTRNYYH 180
Db 162 FRRHCTRNYYH 173

RESULT 35
US-09-826-509-507
; Sequence 507, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brunnsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
```

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; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 507
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-507

Query Match          2.2%; Score 12; DB 12; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRHCTRNYYH 180
Db 162 FRRHCTRNYYH 173

RESULT 36
US-10-225-567A-128
; Sequence 128, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-128

Query Match          2.2%; Score 12; DB 15; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRHCTRNYYH 180
Db 162 FRRHCTRNYYH 173

RESULT 37
US-10-372-095-4
; Sequence 4, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 542
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; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-4

Query Match 2.0%; Score 11; DB 12; Length 542;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 YWILVGLYH 262
Db 236 YWILVGLYH 246
|||||

RESULT 38

US-09-966-871-62

; Sequence 62, Application US/09966871
; Patent No. US20020127539A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Assays for Identifying Receptors Having
; TITLE OF INVENTION: Alterations in Signaling
; FILE REFERENCE: 00398/512002
; CURRENT APPLICATION NUMBER: US/09/966,871
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,302
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/288,644
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-871-62

Query Match 1.8%; Score 10; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TRNYIHMHLF 184
Db 1 TRNYIHMHLF 10
|||||

RESULT 39

US-10-039-645-62

; Sequence 62, Application US/10039645
; Publication No. US20020147170A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; TITLE OF INVENTION: and No. US20020147170A1 functional Receptors as No. US20020147170
; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,550
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-645-62

Query Match 1.8%; Score 10; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TRNYIHMHLF 184
|||||

Db 1 TRNYIHMHLF 10

RESULT 40

US-10-139-084-62
; Sequence 62, Application US/10139084
; Publication No. US20030087313A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Dose Response-Based Methods For
; TITLE OF INVENTION: Identifying Receptors Having Alterations in Signaling
; FILE REFERENCE: 00398/515002
; CURRENT APPLICATION NUMBER: US/10/139,084
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/288,647
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-084-62

Query Match 1.8%; Score 10; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TRNYIHMHLF 184
Db 1 TRNYIHMHLF 10
|||||

RESULT 41

US-10-120-604-11
; Sequence 11, Application US/10120604
; Publication No. US20030096347A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED REC
; TITLE OF INVENTION: HGPBMY28 AND HGPBMY29, AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0143NP
; CURRENT APPLICATION NUMBER: US/10/120,604
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/283,145
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/283,161
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/288,468
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-11

Query Match 1.8%; Score 10; DB 15; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIHM 181
Db 33 LHCTRYIHM 42
|||||

RESULT 42

US-10-010-065-6
; Sequence 6, Application US/10010065

; Publication No. US20020144300A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; APPLICANT: Allen, William
; APPLICANT: Matthews, William
; APPLICANT: Moore, Mark
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING GLUCAGON
; TITLE OF INVENTION: RECEPTOR GENE DISRUPTIONS
; FILE REFERENCE: R-648
; CURRENT APPLICATION NUMBER: US/10/010,065
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,804
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/266,044
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-065-6

Query Match 1.8%; Score 10; DB 14; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
|||||
Db 243 LVEGLYLHNL 252

RESULT 43

US-10-225-567A-134
; Sequence 134, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-134

Query Match 1.8%; Score 10; DB 15; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
|||||
Db 243 LVEGLYLHNL 252

RESULT 44

US-10-225-567A-520
; Sequence 520, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 520
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-520

Query Match 1.8%; Score 10; DB 15; Length 553;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHM 181
|||||
Db 206 LHCTRNYIHM 215

RESULT 45

US-09-966-871-67
; Sequence 67, Application US/09966871
; Patent No. US20020127539A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Assays for Identifying Receptors Having
; TITLE OF INVENTION: Alterations in Signaling
; FILE REFERENCE: 00398/512002
; CURRENT APPLICATION NUMBER: US/09/966,871
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,302
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/288,644
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-871-67

Query Match 1.7%; Score 9; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 RNYIHMHLF 184
|||||
Db 1 RNYIHMHLF 9

RESULT 46

US-10-039-645-67
; Sequence 67, Application US/10039645
; Publication No. US20020147170A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; TITLE OF INVENTION: and No. US20020147170A1functional Receptors as No. US2002014
; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,550
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 10
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-039-645-67

Query Match 1.7%; Score 9; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 RNYIHMHLF 184
Db 1 RNYIHMHLF 9

RESULT 47

US-10-139-084-67
; Sequence 67, Application US/10139084
; Publication No. US20030087313A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Dose Response-Based Methods For
; IDENTIFYING RECEPTORS HAVING ALTERATIONS IN SIGNALING
; FILE REFERENCE: 00398/515002
; CURRENT APPLICATION NUMBER: US/10/139,084
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/288,647
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-084-67

Query Match 1.7%; Score 9; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 RNYIHMHLF 184
Db 1 RNYIHMHLF 9

RESULT 48

US-10-267-730-28
; Sequence 28, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Fotts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-267-730-28

Query Match 1.7%; Score 9; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 FNSFQGFV 409

Db 3 FNSFQGFV 11

RESULT 49

US-10-225-567A-1227
; Sequence 1227, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Roush, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1227
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1227

Query Match 1.7%; Score 9; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 DDILMEKPS 530
Db 12 DDILMEKPS 20

RESULT 50

US-09-935-371-7
; Sequence 7, Application US/09935371
; Patent No. US20020155533A1
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSOYA, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. US20020155533A1
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,371
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,474

```
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-935-371-7

Query Match          1.7%; Score 9; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      183 LFVSFMLRA 191
DB      26 LFVSFMLRA 34
```

Search completed: December 9, 2003, 09:07:45
Job time : 39 secs

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OM protein - protein search, using sw model

Run on: December 9, 2003, 08:58:00 ; Search time 20 Seconds
(without alignments)
2601.363 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGLASLHWGMLMLGSL.....DDLMEKSPRPMSNPDEG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 9616862 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

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Maximum DB seq length: 2000000000

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3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	363	67.1	550	2 A57519	parathyroid hormone
2	25	4.6	585	2 A39286	parathyroid hormone
3	19	3.5	440	2 JC2532	secretin receptor
4	19	3.5	449	2 S16319	secretin receptor
5	18	3.3	589	2 I59297	parathyroid hormone
6	18	3.3	591	2 S44203	parathyroid hormone
7	18	3.3	591	2 I54195	parathyroid hormone
8	18	3.3	593	2 A49191	parathyroid hormone
9	13	2.4	455	2 I53273	gastric inhibitory
10	13	2.4	459	2 JH0594	vasoactive intesti
11	13	2.4	460	2 JC2194	vasoactive intesti
12	13	2.4	462	2 JC2462	gastric inhibitory
13	13	2.4	495	2 JC2195	vasoactive intesti
14	12	2.2	466	2 G02234	gastric inhibitory
15	12	2.2	466	2 S66676	glucose-dependent
16	12	2.2	491	2 I37411	glucose-dependent
17	10	1.8	477	2 JC2041	glucagon receptor
18	9	1.7	381	2 S33449	pituitary adenyilat
19	9	1.7	437	2 JU0185	PACAP/VIP receptor
20	9	1.7	437	2 S39069	vasoactive intesti
21	9	1.7	438	2 G02822	vasoactive intesti
22	9	1.7	463	2 S71624	glucagon-like pept
23	9	1.7	463	2 A46172	glucagon-like pept
24	9	1.7	463	2 I84494	glucagon-like pept
25	9	1.7	467	2 JN0616	pituitary adenyilat
26	9	1.7	485	2 JQ1957	glucagon receptor
27	9	1.7	485	2 JC4363	glucagon receptor
28	9	1.7	495	2 S36114	pituitary adenyilat
29	9	1.7	495	2 S39061	pituitary adenyilat

30 9 1.7 513 2 S47631 pituitary adenyilat
31 9 1.7 523 2 S39060 pituitary adenyilat
32 9 1.7 525 2 JN0902 pituitary adenyilat
33 8 1.5 375 2 I38879 corticotropin rele
34 8 1.5 411 2 A55610 corticotropin rele
35 8 1.5 411 2 S26195 probable carboxyl-
36 8 1.5 415 2 S39535 corticotropin-rele
37 8 1.5 415 2 I58144 corticotropin-rele
38 8 1.5 430 2 A56726 corticotropin-rele
39 8 1.5 431 2 I49279 corticotropin rele
40 8 1.5 431 2 I49149 corticotropin rele
41 8 1.5 444 2 A48260 corticotropin rele
42 8 1.5 533 1 GRBYCP cytosine/purine tr
43 8 1.5 1904 2 T13256 tail-host specific
44 7 1.3 50 2 B37334 L-mandelate dehydr
45 7 1.3 80 2 AB2755 host factor I [imp

ALIGNMENTS

RESULT 1

A57519

parathyroid hormone receptor 2 precursor - human

N/Alternate names: PTH2 receptor

C/Species: Homo sapiens (man)

C/Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999

C/Accession: A57519

R/Usdin, T.B.; Gruber, C.; Bonner, T.I.

J. Biol. Chem. 270, 15455-15458, 1995

A/Title: Identification and functional expression of a receptor selectively recognizi

A/Reference number: A57519; MUID:95318121; PMID:7797535

A/Accession: A57519

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-550 <USD>

A/Cross-references: GB:U25128; NID:9887966; PIDN:AAC50157.1; PID:9887967

C/Genetics:

A/Gene: GDB:PTH2R; PTHR2R

A/Cross-references: GDB:731977; OMIM:601469

A/Map position: 2q33-2q33

C/Superfamily: glucagon receptor

C/Keywords: hormone receptor

Query Match	67.1%;	Score 363;	DB 2;	Length 550;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 463;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	4	LGASHVWGMLGSCLLARAQLDS	DTTIEEQIVLVKAKVQCELNITAOQEGGNC	63
Db	4	LGASHVWGMLGSCLLARAQLDS	DTTIEEQIVLVKAKVQCELNITAOQEGGNC	63
Qy	64	FPWDGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKTWANY	123	
Db	64	FPWDGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKTWANY	123	
Qy	124	DCLRFLOPDISIGKQEFCEFLRYMYTVGYSISFGSLAVAILITGYFERLHCTRNYIEMHL	183	
Db	124	DCLRFLOPDISIGKQEFCEFLRYMYTVGYSISFGSLAVAILITGYFERLHCTRNYIEMHL	183	
Qy	184	FVSPMLRATSFVKDRVVHAHIGVKELESIMQDDPONSIEATSVKDSQYIGCKIAVVMF	243	
Db	184	FVSPMLRATSFVKDRVVHAHIGVKELESIMQDDPONSIEATSVKDSQYIGCKIAVVMF	243	
Qy	244	IYFLATNYTWILVEGLYLHNLIFVAFPSDTKYLGMFFILIGWGFPFAAFVAAMAVARATLAD	303	
Db	244	IYFLATNYTWILVEGLYLHNLIFVAFPSDTKYLGMFFILIGWGFPFAAFVAAMAVARATLAD	303	
Qy	304	ARCWELSGADIKWLYQAPIILAAIGLNIFLNTVRLATKIWNFNVAHGDTRKQYRKLAK	363	
Db	304	ARCWELSGADIKWLYQAPIILAAIGLNIFLNTVRLATKIWNFNVAHGDTRKQYRKLAK	363	
Qy	364	STLVILVLVFGVHYIVFVCLPHSFTGLGWELRMHCELFNSFQGFVSIITCYCNGEVOAE	423	

Db 364 STLVVLVFGVHIVFVCLPHSTGLGWEIRMECELFNSFQGFVSIYCYCNGEVOAE 423
 QY 424 VKQWGRWNLSDVDMKTPPGCGSRRCGSLVLTVTTHSTSSQSQVAA 467
 Db 424 VKQWGRWNLSDVDMKTPPGCGSRRCGSLVLTVTTHSTSSQSQVAA 467

RESULT 2

A39286
 parathyroid hormone / parathyroid hormone-related peptide - North American opossum
 C:Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
 C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 11-Jan-2000
 C:Accession: A39286
 R:Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; K
 Science 254, 1024-1026, 1991
 A:Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-rel
 A:Reference number: A39286; MUID:92054592; PMID:1658941
 A:Accession: A39286
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-585 <UUE>
 A:CROSS-references: GB:M74445
 C:Superfamily: glucagon receptor
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 4.8%; Score 25; DB 2; Length 585;
 Best Local Similarity 100.0%; Pred. No. 6.5e-17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRNYYHMLFVSEMLRA 191
 Db 207 GYFRRLHCTRNYYHMLFVSEMLRA 231

RESULT 3

JC2532
 secretin receptor - human
 C:Species: Homo sapiens (man)
 C>Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
 C:Accession: JC2532
 R:Jiang, S.; Ulrich, C.
 Biochem. Biophys. Res. Commun. 207, 883-890, 1995
 A:Title: Molecular cloning and functional expression of a human pancreatic secretin rece
 A:Reference number: JC2532; MUID:95169147; PMID:7864894
 A:Accession: JC2532
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-440 <UJA>
 A:CROSS-references: EMBL:U20178; NID:9662795; PIDN:AAC50106.1; PID:9662796
 A:Experimental source: pancreas
 C:Genetics:
 A:Gene: GDB:SCTR
 A:CROSS-references: GDB:270546; OMIM:182098
 A:Map position: 2q14.1-2q14.1
 C:Superfamily: glucagon receptor

Query Match 3.5%; Score 19; DB 2; Length 440;
 Best Local Similarity 100.0%; Pred. No. 7e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNYYHMLFVVSF 187
 Db 167 FRRLHCTRNYYHMLFVVSF 185

RESULT 4

S16319
 secretin receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S16319
 R:Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.

EMBO J. 10, 1635-1641, 1991
 A:Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
 A:Reference number: S16319; MUID:91266890; PMID:1646711
 A:Accession: S16319
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-449 <ISH>
 A:CROSS-references: EMBL:X59132; NID:g57228; PIDN:CAA41849.1; PID:g57229
 C:Superfamily: glucagon receptor
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.5%; Score 19; DB 2; Length 449;
 Best Local Similarity 100.0%; Pred. No. 7.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNYYHMLFVVSF 187
 Db 167 FRRLHCTRNYYHMLFVVSF 185

RESULT 5

I59297
 parathyroid hormone/parathyroid hormone related-peptide receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
 C:Accession: I59297
 R:McCuagig, K.A.; Clarke, J.C.; White, J.H.
 Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994
 A:Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parath
 A:Reference number: I59297; MUID:94255468; PMID:8197183
 A:Accession: I59297
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-589 <RES>
 A:CROSS-references: GB:L34611; NID:g530149; PIDN:AAA40011.1; PID:g530151
 C:Genetics:
 A:Gene: PTHR
 A:Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2.
 C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 589;
 Best Local Similarity 100.0%; Pred. No. 9.4e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 Db 290 YFLATNYWILVEGLYLH 307

RESULT 6

S44203
 parathyroid hormone-related peptide receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
 C:Accession: S44203
 R:Karperien, M.; van Dijk, T.B.; Hoeijmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boos
 submitted to the EMBL Data Library, April 1994
 A:Description: Expression pattern of parathyroid hormone/parathyroid hormone related
 A:Reference number: S44203
 A:Accession: S44203
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-591 <KAR>
 A:CROSS-references: EMBL:X78936; NID:g474828; PIDN:CAA55536.1; PID:g474829
 C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 591;
 Best Local Similarity 100.0%; Pred. No. 9.5e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 Db 290 YFLATNYWILVEGLYLH 307

RESULT 7

154195
 A:Title: parathyroid hormone/parathyroid hormone related-peptide receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jan-2000
 C:Accession: I54195; A42698
 R:Paunova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier
 Genomics 20, 20-26, 1994
 A:Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor
 and rat genomes.
 A:Reference number: I54195; MUID:94292182; PMID:8020952
 A:Accession: I54195
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-591 <RES>
 A:Cross-references: GB:L19475; NID:9467316; PIDN:AAA68098.1; PID:9467317
 R:Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure
 Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
 A:Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid
 n of both cAMP and inositol triphosphates and increases intracellular free calcium.
 A:Reference number: A42698; MUID:92212903; PMID:1313566
 A:Accession: A42698
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-585, 'G', 587-591 <ABO>
 A:Experimental source: ROS 17/2.8 osteosarcoma cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:92187)
 C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 591;
 Best Local Similarity 100.0%; Pred. No. 9.5e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 290 YFLATNYWILVEGLYLH 307

RESULT 8

A49191
 A:Title: parathyroid hormone/PTH-related peptide receptor - human
 N:Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor
 C:Species: Homo sapiens (man)
 C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
 C:Accession: I38139; A49191; I38113; G01562; S29610
 R:Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhmann, M.
 Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Juppner, H.
 J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995
 A:Title: Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons
 A:Reference number: I38139; MUID:95263723; PMID:7745008
 A:Accession: I38139
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-593 <RES>
 A:Cross-references: EMBL:U22409; NID:9897594; PIDN:AA860657.1; PID:9897596
 R:Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V.
 Endocrinology 132, 2157-2165, 1993
 A:Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa
 A:Reference number: A49191; MUID:93238641; PMID:8386612
 A:Accession: A49191
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-593 <SCH>
 A:Cross-references: GB:L04308; NID:9190721; PIDN:AAA36525.1; PID:9190722
 A:Note: sequence extracted from NCBI backbone (NCBIN:130233, NCBIP:130234)
 R:Schneider, H.; Feyen, J.H.; Seuwen, K.; Movva, N.R.
 Eur. J. Pharmacol. 246, 149-155, 1993
 A:Title: Cloning and functional expression of a human parathyroid hormone receptor.
 A:Reference number: I38113; MUID:93387403; PMID:8397094
 A:Accession: I38113
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-593 <RES>
 A:Cross-references: EMBL:X68596; NID:9396812; PIDN:CAA48589.1; PID:9396813
 R:Levine, M.
 submitted to the EMBL Data Library, November 1994
 A:Reference number: G07787
 A:Accession: G01562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-593 <LEV>
 A:Cross-references: EMBL:U17418; NID:9596129; PIDN:AAA56774.1; PID:9596130
 C:Genetics:
 A:Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2;
 C:Superfamily: glucagon receptor
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.3%; Score 18; DB 2; Length 593;
 Best Local Similarity 100.0%; Pred. No. 9.5e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 290 YFLATNYWILVEGLYLH 307

RESULT 9

I53273
 A:Title: gastric inhibitory polypeptide receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Sep-1999
 C:Accession: I53273
 R:Ussdin, T.B.; Mezey, E.; Button, D.C.; Brownstein, M.J.; Bonner, T.I.
 Endocrinology 133, 2861-2870, 1993
 A:Title: Gastric inhibitory polypeptide receptor, a member of the secretin-vasoactive
 A:Reference number: I53273; MUID:94062667; PMID:8243312
 A:Accession: I53273
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-455 <RES>
 A:Cross-references: GB:L19660; NID:9431448; PIDN:AAC37637.1; PID:9431449
 C:Superfamily: glucagon receptor

Query Match 2.4%; Score 13; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 9.8e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNVIHM 181
 |||||
 Db 159 FRLHCTRNVIHM 171

RESULT 10

JH0594
 A:Title: vasoactive intestinal peptide receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
 C:Accession: JH0594; S56014
 R:Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
 Neuron 8, 811-819, 1992
 A:Title: Functional expression and tissue distribution of a novel receptor for vasoac
 A:Reference number: JH0594; MUID:92232309; PMID:1314625
 A:Accession: JH0594
 A:Molecule type: mRNA
 A:Residues: 1-459 <ISH>
 A:Cross-references: GB:M86835; NID:9207640; PIDN:AAA42331.1; PID:9207641
 A:Experimental source: lung
 R:Fei, L.; Melmed, S.
 Biochem. J. 308, 719-723, 1995
 A:Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene
 A:Reference number: S56014; MUID:97104266; PMID:8948424
 A:Accession: S56014
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA

A;Residues: 1-26 <PRI>
A;Cross-references: EMBL:U10635; NID:G505752; PIDN:AA848185.1; PID:G514311
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>
F;146-168/Domain: transmembrane #status predicted <TM1>
F;176-195/Domain: transmembrane #status predicted <TM2>
F;218-241/Domain: transmembrane #status predicted <TM3>
F;256-277/Domain: transmembrane #status predicted <TM4>
F;295-318/Domain: transmembrane #status predicted <TM5>
F;344-363/Domain: transmembrane #status predicted <TM6>
F;376-395/Domain: transmembrane #status predicted <TM7>
F;58,69,100,292/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIHMLF 184
|||||
Db 171 LHCTRYIHMLF 183
|||||

RESULT 11
JC2194
vasoactive intestinal peptide receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 07-Oct-1994 #text_change 05-Nov-1999
C;Accession: JC2194; JN0604; PC2289; S38397
R;Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Denis
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A;Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA en
A;Reference number: JC2194; MUID:94235025; PMID:8179610
A;Accession: JC2194
A;Molecule type: mRNA
A;Residues: 1-460 <COU>
A;Cross-references: EMBL:X75299; NID:G407461; PIDN:CAA53046.1; PID:G407462
A;Experimental source: jejunal epithelial cell; clone hIVR8
F;Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.
Biochem. Biophys. Res. Commun. 193, 546-553, 1993
A;Title: Cloning and functional expression of a human neuroendocrine vasoactive intestin
A;Reference number: JN0604; MUID:93290641; PMID:8390245
A;Accession: JN0604
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-284,288-460 <SRE>
A;Cross-references: GB:L13288; NID:G292903; PIDN:AAA36805.1; PID:G292904
R;Couvineau, A.; Gaudin, P.; Maoret, J.J.; Rouyer-Fessard, C.; Nicole, P.; Laburthe, M.
Biochem. Biophys. Res. Commun. 206, 246-252, 1995
A;Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-terminal
A;Reference number: PC2289; MUID:95118345; PMID:7818527
A;Accession: PC2289
A;Molecule type: mRNA
A;Residues: 63-129 <CO2>
C;Genetics:
A;Gene: GDB:VIPR1; RCD1; HVR1
A;Cross-references: GDB:128589; OMIM:192321
A;Map position: 3p22-3p22
C;Superfamily: glucagon receptor
C;Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane pro
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-460/Product: vasoactive intestinal peptide receptor #status predicted <MAT>
F;145-168/Domain: transmembrane #status predicted <TM1>
F;176-194/Domain: transmembrane #status predicted <TM2>
F;216-234/Domain: transmembrane #status predicted <TM3>
F;255-277/Domain: transmembrane #status predicted <TM4>
F;299-319/Domain: transmembrane #status predicted <TM5>
F;346-363/Domain: transmembrane #status predicted <TM6>
F;377-396/Domain: transmembrane #status predicted <TM7>
F;58,69,100,293/Binding site: carboxylate (Asn) (covalent) #status predicted
F;76/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F;250/Binding site: phosphate (Ser) (covalent)

F;450/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIHMLF 184
|||||
Db 170 LHCTRYIHMLF 182
|||||

RESULT 12
JC2462
gastric inhibitory polypeptide receptor - hamster
N;Alternate names: GIP receptor
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2462
R;Yasuda, K.; Inagaki, N.; Yamada, Y.; Kubota, A.; Seino, S.; Seino, Y.
Biochem. Biophys. Res. Commun. 205, 1556-1562, 1994
A;Title: Hamster gastric inhibitory polypeptide receptor expressed in pancreatic isle
A;Reference number: JC2462; MUID:95110292; PMID:7811236
A;Accession: JC2462
A;Molecule type: mRNA
A;Residues: 1-462 <YAS>
A;Cross-references: DDBJ:D38103; NID:G644880; PIDN:BA07284.1; PID:G765087
C;Superfamily: glucagon receptor
C;Keywords: receptor; transmembrane protein
F;136-157/Domain: transmembrane #status predicted <TM1>
F;167-186/Domain: transmembrane #status predicted <TM2>
F;215-238/Domain: transmembrane #status predicted <TM3>
F;252-274/Domain: transmembrane #status predicted <TM4>
F;292-315/Domain: transmembrane #status predicted <TM5>
F;339-357/Domain: transmembrane #status predicted <TM6>
F;383-394/Domain: transmembrane #status predicted <TM7>

Query Match 2.4%; Score 13; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRYIHM 181
|||||
Db 159 FRRLHCTRYIHM 171
|||||

RESULT 13
JC2195
vasoactive intestinal peptide receptor-related protein precursor (clone hIVR5) - hum
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
C;Accession: JC2195; S42087
R;Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-D
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A;Title: Human intestinal VIP receptor: cloning and functional expression of two cDN
A;Reference number: JC2194; MUID:94235025; PMID:8179610
A;Accession: JC2195
A;Molecule type: mRNA
A;Residues: 1-495 <COU>
A;Cross-references: EMBL:X77777; NID:G456352; PIDN:CAA54814.1; PID:G456353
A;Experimental source: jejunal epithelial cell
C;Genetics:
A;Gene: GDB:VIPR1; RCD1; HVR1
A;Cross-references: GDB:128589; OMIM:192321
A;Map position: 3p22-3p22
C;Superfamily: glucagon receptor
C;Keywords: glycoprotein; intestine; phosphoprotein; receptor; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-495/Product: vasoactive intestinal peptide receptor-related protein #status pre
F;180-203/Domain: transmembrane #status predicted <TM1>
F;211-229/Domain: transmembrane #status predicted <TM2>
F;251-269/Domain: transmembrane #status predicted <TM3>
F;290-312/Domain: transmembrane #status predicted <TM4>
F;334-354/Domain: transmembrane #status predicted <TM5>

F:381-398/Domain: transmembrane #status predicted <TM6>
 F:412-431/Domain: transmembrane #status predicted <TM7>
 F:93,104,135,328/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:111/Binding site: phosphate (thr) (covalent) (by protein kinase A) #status predicted
 F:285/Binding site: phosphate (ser) (covalent) (by protein kinase A) #status predicted
 F:485/Binding site: phosphate (ser) (covalent) (by protein kinase C) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIHMLF 184
 |||||
 Db 205 LHCTRYIHMLF 217

RESULT 14

G02234

gastric inhibitory polypeptide receptor - human

N:Alternate names: GIP receptor

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999

A:Accession: G02234

R:Bonner, T.I.; Usdin, T.B.

submitted to the EMBL Data Library, October 1995

A:Reference number: G09336

A:Accession: G02234

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-466 <BON>

A:Cross-references: EMBL:U39231; NID:G1066050; PIDN:AAA84418.1; PID:G1066051

C:Genetics:

A:Gene: GDB:GIPR

A:Cross-references: GDB:335023

A:Map position: 19q13.3-19q13.3

C:Superfamily: glucagon receptor

Query Match 2.2%; Score 12; DB 2; Length 466;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYIH 180
 |||||
 Db 162 FRLHCTRYIH 173

RESULT 15

S66676

glucose-dependent insulinotropic protein receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

A:Accession: S66676

R:Volz, A.; Goetze, R.; Lankat-Buttgereit, B.; Fehmann, H.C.; Bode, H.P.; Goetze, B.

FEBS Lett. 373, 23-29, 1995

A:Title: Molecular cloning, functional expression, and signal transduction of the GIP-re

A:Reference number: S66676; MUID:96013879; PMID:7589426

A:Accession: S66676

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-466 <VOL>

A:Cross-references: GB:S79852

A>Note: the authors translated the codon GCC for residue 427 as Leu

C:Superfamily: glucagon receptor

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-466/Product: Glucose-dependent insulinotropic protein receptor #status predicted <M

Query Match 2.2%; Score 12; DB 2; Length 466;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYIH 180
 |||||
 Db 162 FRLHCTRYIH 173

RESULT 16

I37411

glucose-dependent insulinotropic polypeptide receptor - human

C:Species: Homo sapiens (man)

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Sep-1999

C:Accession: I37411

R:Gremlich, S.; Porret, A.; Hani, E.H.; Cherif, D.; Vionnet, N.; Froguel, P.; Thorens

Diabetes 44, 1202-1208, 1995

A:Title: Cloning, functional expression, and chromosomal localization of the human pa

A:Reference number: I37411; MUID:96007224; PMID:7556958

A:Accession: I37411

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-491 <RES>

A:Cross-references: EMBL:X81832; NID:G1030050; PIDN:CAA57426.1; PID:G1030051

C:Superfamily: glucagon receptor

Query Match 2.2%; Score 12; DB 2; Length 491;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYIH 180
 |||||
 Db 161 FRLHCTRYIH 172

RESULT 17

JC2041

glucagon receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 28-May-1999

C:Accession: JC2041

R:MacNeill, D.J.; Occhi, J.L.; Hey, P.J.; Strader, C.D.; Graziano, M.P.

Biochem. Biophys. Res. Commun. 198, 328-334, 1994

A:Title: Cloning and expression of a human glucagon receptor.

A:Reference number: JC2041; MUID:94121651; PMID:7507321

A:Accession: JC2041

A:Molecule type: mRNA

A:Residues: 1-477 <MAC>

A:Cross-references: GB:U03469; NID:9439689; PIDN:AAC52063.1; PID:9439690

C:Genetics:

A:Gene: GDB:GGR; GGR

A:Cross-references: GDB:304516; OMIM:138033

A:Map position: 17q25-17q25

C:Superfamily: glucagon receptor

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-477/Product: glucagon receptor #status predicted <MAT>

F:143-166/Domain: transmembrane #status predicted <TM1>

F:174-194/Domain: transmembrane #status predicted <TM2>

F:226-244/Domain: transmembrane #status predicted <TM3>

F:266-285/Domain: transmembrane #status predicted <TM4>

F:302-323/Domain: transmembrane #status predicted <TM5>

F:352-369/Domain: transmembrane #status predicted <TM6>

F:386-403/Domain: transmembrane #status predicted <TM7>

F:46,59,74,78/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 1.8%; Score 10; DB 2; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVSEGLYHML 264
 |||||
 Db 243 LVSEGLYHML 252

RESULT 18

S33449

pituitary adenylylate cyclase-activating polypeptide receptor homolog - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000

C:Accession: S33449
 R:svoboda, M.; Ciccarelli, E.; Tastenoy, M.; Christophe, J.
 submitted to the EMBL Data Library, May 1993
 A:Description: Molecular cloning of a PACAP-type receptor.
 A:Reference number: S33449
 A:Accession: S33449
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-381 <SVO>
 A:Cross-references: EMBL:222735; NID:g311228; PIDN:CAA80429.1; PID:g311229
 C:Superfamily: glucagon receptor

Query Match 1.7%; Score 9; DB 2; Length 381;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 LRVSFMLRA 191
 |||||
 Db 77 LRVSFMLRA 85

RESULT 19

JU0185
 PACAP/VIP receptor (PACAPR-3) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
 C:Accession: A53471; JU0185
 R:Inagaki, N.; Yoshida, H.; Mizuta, M.; Mizuno, N.; Fujii, Y.; Gonoi, T.; Miyazaki, J.;
 Proc. Natl. Acad. Sci. U.S.A. 91, 2679-2683, 1994
 A:Title: Cloning and functional characterization of a third pituitary adenylate cyclase-
 A:Reference number: A53471; MUID:94195806; PMID:8146174
 A:Accession: A53471
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-437 <RES>
 A:Cross-references: GB:D28132; NID:g473721; PIDN:BAA05674.1; PID:g496376
 A:Experimental source: strain C57BL/6
 C:Superfamily: glucagon receptor
 C:Keywords: receptor

Query Match 1.7%; Score 9; DB 2; Length 437;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNYYIH 180
 |||||
 Db 153 LHCTRNYYIH 161

RESULT 20

S39069
 vasoactive intestinal peptide receptor VIP2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
 C:Accession: S39069
 R:Lituz, E.M.; Sheward, W.J.; West, K.M.; Morrow, J.A.; Fink, G.; Harmor, A.J.
 FEBS Lett. 334, 3-8, 1993
 A:Title: The VIP(2) receptor: molecular characterization of a cDNA encoding a novel recep
 A:Reference number: S39069; MUID:94039806; PMID:8224221
 A:Accession: S39069
 A:Molecule type: mRNA
 A:Residues: 1-437 <LUT>
 A:Cross-references: EMBL:225885; NID:g414188; PIDN:CAA81104.1; PID:g414189
 C:Superfamily: glucagon receptor
 C:Keywords: G protein-coupled receptor; intestine; transmembrane protein

Query Match 1.7%; Score 9; DB 2; Length 437;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNYYIH 180
 |||||
 Db 153 LHCTRNYYIH 161

RESULT 21

G02822
 vasoactive intestinal peptide receptor 2 - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Jun-2000
 C:Accession: G02822; JC2463
 R:Lituz, E.M.
 submitted to the EMBL Data Library, January 1996
 A:Reference number: H01736
 A:Accession: G02822
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-438 <LUT>
 A:Cross-references: EMBL:X95097; NID:g1160469; PIDN:CAA64474.1; PID:g1160470
 R:svoboda, M.; Tastenoy, M.; Van Rampelbergh, J.; Goossens, J.F.; De Neef, P.; Waelbr
 Biochem. Biophys. Res. Commun. 205, 1617-1624, 1994
 A:Title: Molecular cloning and functional characterization of a human VIP receptor fr
 A:Reference number: JC2463; MUID:95110300; PMID:7811244
 A:Accession: JC2463
 A:Molecule type: mRNA
 A:Residues: 1-38, 'T', '40-411, 'H', '413-423, 'A', '425-438 <SVO>
 A:Cross-references: GB:L36566; NID:g550477; PIDN:AAC37569.1; PID:g550478
 A:Experimental source: SUP-T1 lymphoblast cell line
 C:Genetics:

A:Gene: GDB:VIPR2
 A:Cross-references: GDB:335025
 A:Map position: 7q36.3-7q36.3
 C:Superfamily: glucagon receptor
 C:Keywords: glycoprotein; intestine; receptor; transmembrane protein
 F:160-179/Domain: transmembrane #status predicted <TM1>
 F:130-150/Domain: transmembrane #status predicted <TM2>
 F:206-228/Domain: transmembrane #status predicted <TM3>
 F:241-262/Domain: transmembrane #status predicted <TM4>
 F:282-304/Domain: transmembrane #status predicted <TM5>
 F:329-349/Domain: transmembrane #status predicted <TM6>
 F:361-384/Domain: transmembrane #status predicted <TM7>
 F:58,88,92/Binding site: carbohydrate (Asn) #status predicted

Query Match 1.7%; Score 9; DB 2; Length 438;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNYYIH 180
 |||||
 Db 154 LHCTRNYYIH 162

RESULT 22

S71624
 Glucagon-like peptide-1 receptor, pancreatic - human
 N:Alternate names: GLP-1-receptor
 C:Species: Homo sapiens (man)
 C:Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 17-Nov-2000
 C:Accession: S71624; JN0807; I38398; I84485; S45707
 R:Wei, Y.; Molisov, S.
 FEBS Lett. 358, 219-224, 1995
 A:Title: Tissue-specific expression of the human receptor for glucagon-like peptide-1
 A:Reference number: S71624; MUID:95145713; PMID:7843404
 A:Accession: S71624
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-463 <WEI>
 A:Cross-references: EMBL:U10037; NID:g717033; PIDN:AAA63787.1; PID:g717034
 A:Experimental source: clone HPC10; pancreas
 R:Graziano, M.P.; Hey, P.J.; Borkowski, D.; Chicchi, G.G.; Strader, C.D.
 Biochem. Biophys. Res. Commun. 196, 141-146, 1993
 A:Title: Cloning and functional expression of a human glucagon-like peptide-1 recept
 A:Reference number: JN0807; MUID:94029985; PMID:8216285
 A:Accession: JN0807
 A:Molecule type: mRNA
 A:Residues: 1-220, 'Q', '222-463 <GRA>

A;Cross-references: GB:I23503; NID:G402480; PIDN:AAAI7021.1; PID:G402481
 A;Experimental source: gastric tumor cell
 R;Dillon, J.S.; Tanizawa, Y.; Wheeler, M.B.; Leng, X.H.; Ligon, B.B.; Rabin, D.U.; Yoo-W
 Endocrinology 133, 1907-1910, 1993
 A;Title: Cloning and functional expression of the human glucagon-like peptide-1 (GLP-1)
 A;Reference number: I38398; MUID:94008746; PMID:8404634
 A;Accession: I38398
 A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-220, 'Q', 222-259, 'F', 261-315, 'G', 317-463 <RES>
 A;Cross-references: EMBL:U01157; NID:9684918; PIDN:AAAG2471.1; PID:G933108
 A;Accession: I84485
 A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-220, 'Q', 222-259, 'F', 261-315, 'G', 317-463 <RE2>
 A;Cross-references: EMBL:U01156; NID:G933105; PIDN:AAAC50050.1; PID:G933106
 R;van Eyll, B.; Lankat-Buttgeit, B.; Bode, H.P.; Goeke, R.; Goeke, B.
 FEBS Lett. 348, 7-13, 1994
 A;Title: Signal transduction of the GLP-1-receptor cloned from a human insulinoma.
 A;Reference number: S45707; MUID:94298957; PMID:7517895
 A;Accession: S45707
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-11, 'V', 13-136, 'R', 138-220, 'Q', 222-259, 'F', 261-463 <BYL>
 C;Comment: This protein acts the stimulation of adenylyl cyclase to raise intracellular
 C;Function:
 A;Description: stimulates glucose-induced insulin secretion
 C;Superfamily: Glucagon receptor
 C;Keywords: G protein-coupled receptor; glycoprotein; pancreas; transmembrane protein
 F;146-169/Domain: transmembrane #status predicted <TM1>
 F;177-196/Domain: transmembrane #status predicted <TM2>
 F;228-246/Domain: transmembrane #status predicted <TM3>
 F;268-287/Domain: transmembrane #status predicted <TM4>
 F;304-325/Domain: transmembrane #status predicted <TM5>
 F;352-371/Domain: transmembrane #status predicted <TM6>
 F;388-407/Domain: transmembrane #status predicted <TM7>
 F;63,82,115/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 1.7%; Score 9; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 172 LHCTRNYYH 180
 DB 172 LHCTRNYYH 180
 RESULT 23
 A46172
 Glucagon-like peptide 1 receptor - rat
 N;Alternate names: GLP-1 receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text_change 24-Sep-1999
 C;Accession: A46172; I53420; I59231
 R;Thorens, B.
 Proc. Natl. Acad. Sci. U.S.A. 89, 8641-8645, 1992
 A;Title: Expression cloning of the pancreatic beta cell receptor for the gluco-incretin
 A;Reference number: A46172; MUID:92409572; PMID:1326760
 A;Accession: A46172
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-463 <THO>
 A;Cross-references: GB:M97797; NID:G204326; PIDN:AAAT3377.1; PID:G387868
 A;Experimental source: pancreatic islet cells
 A;Note: sequence extracted from NCBI backbone
 R;Lankat-Buttgeit, B.; Goke, R.; Fehmann, H.C.; Richter, G.; Goke, B.
 Exp. Clin. Endocrinol. 102, 341-347, 1994
 A;Title: Molecular cloning of a cDNA encoding for the GLP-1 receptor expressed in rat lu
 A;Reference number: I53420; MUID:95112989; PMID:7813606
 A;Accession: I53420
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-322, 'I', 324-463 <RES>

A;Cross-references: GB:S75952; NID:G913834
 C;Superfamily: glucagon receptor
 C;Keywords: transmembrane protein
 Query Match 1.7%; Score 9; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 172 LHCTRNYYH 180
 DB 172 LHCTRNYYH 180
 RESULT 24
 I84494
 glucagon-like peptide-1 receptor - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 24-Sep-1999
 C;Accession: I84494
 R;Thorens, B.; Porret, A.; Buehler, L.; Deng, S.; Morel, P.; Widmann, C.
 Diabetes 42, 1678-1682, 1993
 A;Title: Cloning and functional expression of the human islet GLP-1 receptor. Demonst
 A;Reference number: I38653; MUID:94009966; PMID:8405712
 A;Accession: I84494
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-463 <RES>
 A;Cross-references: EMBL:U01104; NID:G405081; PIDN:AAA03614.1; PID:G405082
 C;Genetics:
 A;Gene: GDB:GLP1R
 A;Cross-references: GDB:I37218; OMIM:I38032
 A;Map position: 6p21-6p21
 C;Superfamily: glucagon receptor
 Query Match 1.7%; Score 9; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 172 LHCTRNYYH 180
 DB 172 LHCTRNYYH 180
 RESULT 25
 JN0616
 pituitary adenylate cyclase-activating polypeptide receptor 46-5 precursor - rat
 N;Alternate names: PACAP receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 08-Oct-1999
 C;Accession: JN0616; S36768
 R;Hosoya, M.; Onda, H.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ohtaki, T.; Okazaki, H.; A
 Biochem. Biophys. Res. Commun. 194, 133-143, 1993
 A;Title: Molecular cloning and functional expression of rat cDNAs encoding the recept
 A;Reference number: JN0616; MUID:93326107; PMID:7687425
 A;Accession: JN0616
 A;Molecule type: mRNA
 A;Residues: 1-467 <HOS>
 A;Experimental source: brain
 R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holtsboer, F.; Bockaert, J.; Seeburg, P.H.;
 Nature 365, 170-175, 1993
 A;Title: Differential signal transduction by five splice variants of the PACAP recept
 A;Reference number: S36768; MUID:93382505; PMID:8396727
 A;Accession: S36768
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-467 <SPE>
 A;Cross-references: EMBL:Z33279; NID:G404252; PIDN:CAAS0817.1; PID:G404253
 C;Superfamily: glucagon receptor
 C;Keywords: alternative splicing; glycoprotein; receptor
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-467/Product: pituitary adenylate cyclase-activating polypeptide receptor 46-5 #s
 F;47,59,116,299,342,374/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.7%; Score 9; DB 2; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSEMLRA 191
 |||||
 Db 191 LFVSEMLRA 199

RESULT 26
 JQ1957
 glucagon receptor - rat
 N/Alternate names: GIP-1 receptor homolog, hepatic
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
 C/Accession: JQ1957; A46211; S29689
 R/Svoboda, M.; Ciccarelli, E.; Tastenoy, M.; Cauvin, A.; Stievenart, M.; Charistophe, J.
 Biochem. Biophys. Res. Commun. 191, 479-486, 1993
 A/Title: Small introns in a hepatic cDNA encoding a new glucagon-like peptide 1-type rec
 A/Reference number: JQ1957; MUID:93213282; PMID:8384842
 A/Accession: JQ1957
 A/Molecule type: mRNA
 A/Residues: 1-485 <SVO>
 A/Cross-references: GB:X68692
 A/Experimental source: liver
 R/Jelinek, L.J.; Lok, S.; Rosenberg, G.B.; Smith, R.A.; Grant, F.J.; Biggs, S.; Bensch,
 nman, P.A.; Kindsvogel, W.
 Science 259, 1614-1616, 1993
 A/Title: Expression cloning and signaling properties of the rat glucagon receptor.
 A/Reference number: A46211; MUID:93206096; PMID:8384375
 A/Accession: A46211
 A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A/Molecule type: mRNA
 A/Residues: 1-37,'W',38-215,'W',217-323,'V',325-485 <JEL>
 A/Experimental source: liver
 A/Note: sequence extracted from NCBI backbone (NCBIP:127785)
 C/Genetics:
 A/Introns: 132/3; 168/2; 220/3; 407/3
 C/Superfamily: glucagon receptor
 C/Keywords: G protein-coupled receptor; glycoprotein; liver; phosphoprotein; transmembra
 F:144-167/Domain: transmembrane #status predicted <TM1>
 F:175-194/Domain: transmembrane #status predicted <TM2>
 F:227-251/Domain: transmembrane #status predicted <TM3>
 F:264-286/Domain: transmembrane #status predicted <TM4>
 F:305-324/Domain: transmembrane #status predicted <TM5>
 F:352-370/Domain: transmembrane #status predicted <TM6>
 F:389-405/Domain: transmembrane #status predicted <TM7>
 F:47,60,75,79/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:432/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 1.7%; Score 9; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYYH 180
 |||||
 Db 170 LHCTRNYYH 178

RESULT 27
 JC4363
 glucagon receptor precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 21-Jul-2000
 C/Accession: JC4363
 R/Burcelin, R.; Li, J.; Charron, M.J.
 Gene 164, 305-310, 1995
 A/Title: Cloning and sequence analysis of the murine glucagon receptor-encoding gene.
 A/Reference number: JC4363; MUID:96069600; PMID:7590348
 A/Accession: JC4363
 A/Molecule type: mRNA
 A/Residues: 1-485 <EUR>
 A/Cross-references: GB:L38612; NID:G7274387; PIDN:AAF44749.1; PID:G7274388

C/Comment: This receptor is a plasma membrane glycoprotein that belongs to a subfamily
 genolysis and gluconeogenesis in li ver and insulin secretion by beta cells.
 C/Genetics:
 A/Gene: gr
 A/Introns: 21/3; 55/1; 91/1; 132/3; 168/2; 220/3; 273/1; 294/2; 317/3; 347/2; 393/3;
 C/Superfamily: glucagon receptor
 C/Keywords: glycoprotein; receptor; transmembrane protein
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-485/Product: glucagon receptor #status predicted <MAT>
 F:145-168/Domain: transmembrane #status predicted <TM1>
 F:176-196/Domain: transmembrane #status predicted <TM2>
 F:225-239/Domain: transmembrane #status predicted <TM3>
 F:247-258/Domain: transmembrane #status predicted <TM4>
 F:266-288/Domain: transmembrane #status predicted <TM5>
 F:304-331/Domain: transmembrane #status predicted <TM6>
 F:354-369/Domain: transmembrane #status predicted <TM7>
 F:386-405/Domain: transmembrane #status predicted <TM8>
 F:47,60,65,75,79,118/Binding site: carboxylate (Asn) (covalent) #status predicted
 Query Match 1.7%; Score 9; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYYH 180
 |||||
 Db 170 LHCTRNYYH 178

RESULT 28
 S36114
 pituitary adenylate cyclase-activating polypeptide type I receptor precursor - rat
 N/Alternate names: PACAP receptor
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
 C/Accession: S36114; JN0617; S39062; S39063; PNO608; PNO609; I58147; A48204
 R/Morrow, J.A.; Lutz, E.M.; West, K.M.; Fink, G.; Harmar, A.J.
 FEBS Lett. 329, 99-105, 1993
 A/Title: Molecular cloning and expression of a cDNA encoding a receptor for pituitary
 A/Reference number: S36114; MUID:93359075; PMID:8394834
 A/Accession: S36114
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-495 <MOR>
 A/Cross-references: EMBL:Z23282; NID:G397520; PIDN:CAA80820.1; PID:G397521
 R/Hosoya, M.; Onda, H.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ohkaki, T.; Okazaki, H.; ;
 Biochem. Biophys. Res. Commun. 194, 133-143, 1993
 A/Title: Molecular cloning and functional expression of rat cDNAs encoding the recep
 A/Reference number: JN0616; MUID:93326107; PMID:7687425
 A/Accession: JN0617
 A/Molecule type: mRNA
 A/Residues: 1-495 <HOS>
 A/Experimental source: brain
 R/Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.
 Nature 365, 170-175, 1993
 A/Title: Differential signal transduction by five splice variants of the PACAP recep
 A/Reference number: S36768; MUID:93382505; PMID:8396727
 A/Accession: S39062
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-495 <SPE>
 A/Cross-references: EMBL:Z23274; NID:G404220; PIDN:CAA80812.1; PID:G404221
 A/Accession: S39063
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-348,350-495 <SP2>
 A/Cross-references: EMBL:Z23275; NID:G404197; PIDN:CAA80813.1; PID:G404198
 R/Svoboda, M.; Tastenoy, M.; Ciccarelli, E.; Stievenart, M.; Christophe, J.
 Biochem. Biophys. Res. Commun. 195, 881-888, 1993
 A/Title: Cloning of a splice variant of the pituitary adenylate cyclase-activating p
 A/Reference number: PNO608; MUID:93384616; PMID:8396930
 A/Accession: PNO608
 A/Molecule type: mRNA
 A/Residues: 78-495 <SVO>

A;Accession: PM0609
 A;Molecule type: protein
 A;Residues: 349-376 <SV2>
 R;Hashimoto, H.; Ishihara, T.; Shigemoto, R.; Mori, K.; Nagata, S.
 Neuron 11, 333-342, 1993
 A;Title: Molecular cloning and tissue distribution of a receptor for pituitary adenylate cyclase-activating polypeptide type I (cattle)
 A;Reference number: 158147; MUID:93357025; PMID:8394723
 A;Accession: 158147
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-495 <RES>
 A;Cross-references: GB:D16465; NID:G440381; PIDN:BA03932.1; PID:G457661
 R;Pisegna, J.R.; Wank, S.A.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6345-6349, 1993
 A;Title: Molecular cloning and functional expression of the pituitary adenylate cyclase-activating polypeptide type I receptor
 A;Reference number: A48204; MUID:93317678; PMID:8392197
 A;Accession: A48204
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-420, 'L', 422-495 <PIS>
 A;Cross-references: GB:L16680; NID:G347941; PIDN:AAA41792.1; PID:G347942
 C;Comment: This protein stimulates both adenylate cyclase and phospholipase C and dually C;Superfamily: glucagon receptor
 C;Keywords: alternative splicing; anterior pituitary; G protein-coupled receptor; glycoprotein; pituitary adenylate cyclase-activating polypeptide receptor long form # F1-347,376-495/Product: pituitary adenylate cyclase-activating polypeptide receptor short form # F1-19/Domain: signal sequence #status predicted <SIG>
 F1-20-495/Product: pituitary adenylate cyclase-activating polypeptide type I receptor #status predicted <TM1>
 F186-204/Domain: transmembrane #status predicted <TM2>
 F1227-252/Domain: transmembrane #status predicted <TM3>
 F1268-290/Domain: transmembrane #status predicted <TM4>
 F308-331/Domain: transmembrane #status predicted <TM5>
 F378-398/Domain: transmembrane #status predicted <TM6>
 F413-433/Domain: transmembrane #status predicted <TM7>
 F47,59,116,299,342,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F365,444/Binding site: phosphate (Ser) (covalent) #status predicted
 Query Match 1.7%; Score 9; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 LFVSFMLRA 191
 DB 191 LFVSFMLRA 199
 RESULT 29
 S39061
 pituitary adenylate cyclase activating-peptide receptor form 3 - rat
 N;Alternate names: PACAP receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
 C;Accession: S39061
 R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.; Jørgensen, J.S.
 Nature 365, 170-175, 1993
 A;Title: Differential signal transduction by five splice variants of the PACAP receptor.
 A;Reference number: S36768; MUID:93382505; PMID:8396727
 A;Accession: S39061
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-495 <SPE>
 A;Cross-references: EMBL:D23273; NID:G404210; PIDN:CAA080811.1; PID:G404211
 C;Superfamily: glucagon receptor

Query Match 1.7%; Score 9; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSFMLRA 191
 DB 191 LFVSFMLRA 199

RESULT 30
 S47631
 pituitary adenylate cyclase-activating polypeptide type I receptor precursor - bovine
 N;Alternate names: PACAP receptor
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
 C;Accession: S47631; S47632
 R;Miyamoto, Y.; Habata, Y.; Ohtaki, T.; Masuda, Y.; Ogi, K.; Onda, H.; Fujino, M.
 Biochim. Biophys. Acta 1218, 297-307, 1994
 A;Title: Cloning and expression of a complementary DNA encoding the bovine receptor for pituitary adenylate cyclase-activating polypeptide type I
 A;Reference number: S47631; MUID:94325336; PMID:8049255
 A;Accession: S47631
 A;Molecule type: mRNA
 A;Residues: 1-513 <MIY>
 A;Cross-references: EMBL:D17290; NID:G602765; PIDN:BA04122.1; PID:G1374682
 A;Experimental source: brain
 A;Accession: S47632
 A;Molecule type: protein
 A;Residues: 38-41, 'X', 43-50, 'X', 52-66 <MI2>
 A;Experimental source: brain
 C;Genetics: 366/2
 C;Function:
 A;Description: stimulates both adenylate cyclase and phospholipase C
 C;Superfamily: glucagon receptor
 C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; phosphoprotein; pituitary adenylate cyclase-activating polypeptide type I receptor
 F1-37/Domain: signal sequence #status predicted <SIG>
 F38-385,394-513/Product: pituitary adenylate cyclase-activating polypeptide type I receptor #status predicted <TM1>
 F173-195/Domain: transmembrane #status predicted <TM2>
 F204-222/Domain: transmembrane #status predicted <TM3>
 F245-270/Domain: transmembrane #status predicted <TM4>
 F286-308/Domain: transmembrane #status predicted <TM5>
 F326-349/Domain: transmembrane #status predicted <TM6>
 F396-416/Domain: transmembrane #status predicted <TM7>
 F431-451/Domain: transmembrane #status predicted <TM8>
 F65,77,134,360,420/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F383,462/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 1.7%; Score 9; DB 2; Length 513;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSFMLRA 191
 DB 209 LFVSFMLRA 217

RESULT 31
 S39060
 pituitary adenylate cyclase activating-peptide receptor form 2 - rat
 N;Alternate names: PACAP receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 C;Accession: S39060
 R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.; Jørgensen, J.S.
 Nature 365, 170-175, 1993
 A;Title: Differential signal transduction by five splice variants of the PACAP receptor.
 A;Reference number: S36768; MUID:93382505; PMID:8396727
 A;Accession: S39060
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-523 <SPE>
 A;Cross-references: EMBL:D23272; NID:G404195; PIDN:CAA080810.1; PID:G404196
 C;Superfamily: glucagon receptor

Query Match 1.7%; Score 9; DB 2; Length 523;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSFMLRA 191

Db 191 LFVSEMLRA 199
|||||

RESULT 32

JN0902
pituitary adenylate cyclase activating peptide receptor type I precursor - human
C:Species: Homo sapiens (man)
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Jun-2000
C:Accession: JN0902
R:Ogi, K.; Miyamoto, Y.; Masuda, Y.; Habata, Y.; Hosoya, M.; Ohtaki, T.; Masuo, Y.; Onda
Biochem. Biophys. Res. Commun. 196, 1511-1521, 1993
A:Title: Molecular cloning and functional expression of a cDNA encoding a human pituitary
A:Reference number: JN0902; MUID:94071918; PMID:7902709
A:Accession: JN0902

A:Molecule type: mRNA
A:Residues: 1-525 <OGI>
A:Cross-references: DDBJ:D17516; NID:9457562; PIDN:BAA04466.1; PID:9540518
A:Experimental source: pituitary
C:Comment: This protein plays pivotal roles as a neurotransmitter and a neuromodulator,
C:Superfamily: glucagon receptor
C:Keywords: glycoprotein; neurotransmitter; receptor
F:1-77/Domain: signal sequence #status predicted <SIG>
F:78-525/Product: pituitary adenylate cyclase activating peptide receptor type I #status
F:105,117,174,357,400,432/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.7%; Score 9; DB 2; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSEMLRA 191
|||||
Db 249 LFVSEMLRA 257

RESULT 33

I38879
corticotropin releasing hormone receptor variant - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I38879
R:Ross, P.C.; Kostas, C.M.; Ramabhadran, T.V.
Biochem. Biophys. Res. Commun. 205, 1836-1842, 1994
A:Title: A variant of the human corticotropin-releasing factor (CRF) receptor: cloning,
A:Reference number: I38879; MUID:95110332; PMID:7811272
A:Accession: I38879
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-375 <RES>
A:Cross-references: EMBL:U16273; NID:9606973; PIDN:AAC50073.1; PID:9606974
C:Superfamily: glucagon receptor

Query Match 1.5%; Score 8; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVFS 410
|||||
Db 313 SFQGFVFS 320

RESULT 34

A55610
corticotropin-releasing factor receptor subtype 2 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
C:Accession: A55610
R:Lovenberg, T.W.; Liaw, C.W.; Grigoriadis, D.E.; Cleverger, W.; Chalmers, D.T.; De Souza
Proc. Natl. Acad. Sci. U.S.A. 92, 836-840, 1995
A:Title: Cloning and characterization of a functionally distinct corticotropin-releasing
A:Reference number: A55610; MUID:95148632; PMID:7846062
A:Accession: A55610
A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA
A:Residues: 1-411 <LOV>
A:Cross-references: EMBL:U16253; NID:9644771; PIDN:AAC52159.1; PID:9644772
C:Genetics:
A:Gene: CRF2R
C:Superfamily: glucagon receptor

Query Match 1.5%; Score 8; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVFS 410
|||||
Db 349 SFQGFVFS 356

RESULT 35

S26195
probable carboxyl-terminal processing proteinase - *Synechococcus* sp. (PCC 7002) (frag
C:Species: *Synechococcus* sp.
A:Variety: PCC 7002
C>Date: 07-May-1998 #sequence_revision 17-Jul-1998 #text_change 29-Sep-1999
C:Accession: S26195; S18125
R:Brand, S.N.; Tan, X.; Widger, W.R.
Plant Mol. Biol. 20, 481-491, 1992
A:Title: Cloning and sequencing of the petBD operon from the cyanobacterium *Synechococ
A:Reference number: S26193; MUID:93043038; PMID:1421151
A:Accession: S26195
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-411 <BRA>
A:Cross-references: EMBL:X63049; NID:938962; PIDN:CAA44776.1; PID:938965
C:Superfamily: carboxyl-terminal processing proteinase*

Query Match 1.5%; Score 8; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 LVLVLVFG 373
|||||
Db 15 LVLVLVFG 22

RESULT 36

S39535
corticotropin-releasing hormone receptor - mouse
C:Species: *Mus musculus* (house mouse)
C>Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
C:Accession: S39535
R:Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.
FEBS Lett. 335, 1-5, 1993
A:Title: Primary structure and functional expression of mouse pituitary and human bra
A:Reference number: S39534; MUID:94063063; PMID:8243652
A:Accession: S39535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-415 <VIT>
A:Cross-references: EMBL:X72305; NID:9436120; PIDN:CAA51053.1; PID:9436121
A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 1.5%; Score 8; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVFS 410
|||||
Db 353 SFQGFVFS 360

RESULT 37

I58144

corticotropin-releasing factor receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C;Accession: I58144
R;Chang, C.P.; Pearce, R.V.; O'Connell, S.; Rosenfeld, M.G.
Neuron 11, 1187-1195, 1993
A;Title: Identification of a seven transmembrane helix receptor for corticotropin-releasing factor
A;Reference number: I58144; MUID:9409969; PMID:8274282
A;Accession: I58144
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-415 <RES>
A;Cross-references: GB:I25438; NID:9450298; PIDN:AAAL6441.1; PID:9457615
C;Superfamily: glucagon receptor

Query Match 1.5%; Score 8; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
|||||
DB 353 SFQGFVVS 360

RESULT 38

A56726
corticoliberin receptor precursor, cardiac - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 24-Nov-1999
C;Accession: A56726
R;Stenzel, P.; Kesterson, R.; Yeung, W.; Cone, R.D.; Rittenberg, M.B.; Stenzel-Poore, M.
Mol. Endocrinol 9, 637-645, 1995
A;Title: Identification of a novel murine receptor for corticotropin-releasing hormone
A;Reference number: A56726; MUID:96015396; PMID:7565810
A;Accession: A56726
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-430 <STE>
A;Cross-references: GB:U19939; NID:9806763; PIDN:AAC52243.1; PID:9806764
C;Superfamily: glucagon receptor
C;Keywords: cardiac muscle; heart

Query Match 1.5%; Score 8; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
|||||
DB 368 SFQGFVVS 375

RESULT 39

I49279
sauvagine/corticotropin-releasing factor receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I49279
R;Kishimoto, T.; Pearce, R.V.
Proc. Natl. Acad. Sci. U.S.A. 92, 1108-1112, 1995
A;Title: A sauvagine/corticotropin-releasing factor receptor expressed in heart and skeletal muscle
A;Reference number: I49279; MUID:95166778; PMID:7755719
A;Accession: I49279
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-431 <KIS>
A;Cross-references: EMBL:U21729; NID:9717137; PIDN:AAC52174.1; PID:9717138
C;Superfamily: glucagon receptor

Query Match 1.5%; Score 8; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410

DB 369 SFQGFVVS 376
|||||

RESULT 40

I49149
CRF receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
C;Accession: I49149
R;Perrin, M.; Donaldson, C.; Chen, R.; Blount, A.; Berggren, T.; Bilezikian, L.; Saw
Proc. Natl. Acad. Sci. U.S.A. 92, 2969-2973, 1995
A;Title: Identification of a second corticotropin-releasing factor receptor gene and
A;Reference number: I49149; MUID:95224061; PMID:7708757
A;Accession: I49149
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-431 <RES>
A;Cross-references: EMBL:U17858; NID:9727254; PIDN:AAA68026.1; PID:9727255
C;Superfamily: glucagon receptor

Query Match 1.5%; Score 8; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
|||||
DB 369 SFQGFVVS 376

RESULT 41

A48250
corticoliberin receptor, long splice form - human
N;Alternate names: corticoliberin binding protein; corticotropin releasing factor rec
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 11-Apr-1997 #text_change 21-Jul-2000
C;Accession: I60975; A48260; S39534
R;Chen, R.; Lewis, K.A.; Perrin, M.H.; Vale, W.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 8967-8971, 1993
A;Title: Expression cloning of a human corticotropin-releasing factor (CRF) receptor.
A;Reference number: A48260; MUID:94022296; PMID:7692441
A;Accession: I60975
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-444 <RES>
A;Cross-references: GB:I23333; NID:9408691; PIDN:AAA35719.1; PID:9408692
A;Experimental source: Cushing corticotropic cell tumor
A;Accession: A48260
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-145,175-444 <RE2>
A;Cross-references: GB:I23332; NID:9408689; PIDN:AAA35718.1; PID:9408690
R;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.
FEBS Lett. 335, 1-5, 1993
A;Title: Primary structure and functional expression of mouse pituitary and human bra
A;Reference number: S39534; MUID:94063063; PMID:8243652
A;Accession: S39534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-145,175-444 <VIT>
A;Cross-references: EMBL:X72304; NID:9436118; PIDN:CAA51052.1; PID:9436119
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an a
C;Genetics:
A;Gene: GDB:CRHR1; CRHR; CRF-R; CRF1
A;Cross-references: GDB:235922; OMIM:122561
A;Map position: 17q12-17q22
C;Superfamily: glucagon receptor
C;Keywords: alternative splicing; transmembrane protein

Query Match 1.5%; Score 8; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVS 410
 |||||
 Db 382 SFQGFVS 389

RESULT 42

GRBYCP

cytosine/purine transport protein - yeast (Saccharomyces cerevisiae)

N;Alternate names: cytosine/purine permease; protein YER0566

C;Species: Saccharomyces cerevisiae

C;Date: 31-Dec-1992 #sequence_revision 19-May-1995 #text_change 05-Nov-1999

C;Accession: S50559; S20153

R;Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A;Description: The sequence of S. cerevisiae lambda clones 6592, 4678, 4742, and 3612.

A;Reference number: S50557

A;Accession: S50559

A;Molecule type: DNA

A;Residues: 1-533 <DIE>

A;Cross-references: EMBL:U18813; NID:G1381127; PIDN:AAB64592.1; PID:G603292; GSPDB:GN000

A;Experimental source: strain S288c (AB972)

R;Weber, E.; Rodriguez, C.; Chevallerier, M.R.; Jund, R.

Mol. Microbiol. 4, 585-596, 1990

A;Title: The purine-cytosine permease gene of Saccharomyces cerevisiae: primary structure

A;Reference number: S20153; MUID:90279501; PMID:2191181

A;Accession: S20153

A;Molecule type: DNA

A;Residues: 1-191, 'M', 193-260, 'G', 262-533 <WEB>

A;Cross-references: EMBL:X51751; NID:93699; PIDN:CAA36040.1; PID:G3700

A;Experimental source: strain FL100

C;Genetics:

A;Gene: SGD:FCY2; MIPS:YER0566

A;Cross-references: SGD:S0000858; MIPS:YER0566

A;Map position: 5R

C;Superfamily: cytosine/purine transport protein

C;Keywords: Glycoprotein; transmembrane protein

F;99-119/Domain: transmembrane #status predicted <TM1>

F;122-142/Domain: transmembrane #status predicted <TM2>

F;143-198/Domain: extracellular #status predicted <EXT>

F;199-221/Domain: transmembrane #status predicted <TM3>

F;257-277/Domain: transmembrane #status predicted <TM4>

F;301-320/Domain: transmembrane #status predicted <TM5>

F;345-368/Domain: transmembrane #status predicted <TM6>

F;398-419/Domain: transmembrane #status predicted <TM7>

F;466-485/Domain: transmembrane #status predicted <TM8>

F;160,181/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 1.58; Score 8; DB 1; Length 533;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 LIFVAFPS 271

|||||

Db 133 LIFVAFPS 140

RESULT 43

T13256

tail-host specificity protein homolog - Lactococcus lactis phage BK5-T

C;Species: Lactococcus lactis phage BK5-T

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999

C;Accession: T13256

R;Boyce, J.D.; Davidson, B.E.; Hillier, A.J.

Appl. Environ. Microbiol. 61, 4089-4098, 1995

A;Title: Sequence analysis of the temperate Lactococcus lactis bacteriophage BK5-T and d

A;Reference number: Z17646; MUID:96064422; PMID:8526523

A;Accession: T13256

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1904 <BOY>

A;Cross-references: EMBL:L44593; NID:9928826; PID:9928828; PIDN:AAA98579.1

Query Match

Best Local Similarity 1.58; Score 8; DB 2; Length 1904;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVS 410

|||||

Db 1773 SFQGFVS 1780

RESULT 44

B37334

L-mandelate dehydrogenase (EC 1.1.2.-) - Acinetobacter calcoaceticus (fragment)

C;Species: Acinetobacter calcoaceticus

C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 13-Sep-1998

C;Accession: B37334

R;Ferguson, C.A.

submitted to the Protein Sequence Database, October 1992

A;Reference number: A37334

A;Accession: B37334

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-50 <FEW>

C;Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology

C;Keywords: oxidoreductase

Query Match

Best Local Similarity 1.3%; Score 7; DB 2; Length 50;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 KLAESTL 366

|||||

Db 12 KLAESTL 18

RESULT 45

AB2755

host factor I [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

C;Accession: AB2755

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moc

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McCl

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kan

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AB2755

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-80 <KUR>

A;Cross-references: GB:AE008688; PIDN:AAL42456.1; PID:G17739871; GSPDB:GN00186

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: hfg

A;Map position: circular chromosome

C;Superfamily: host factor I

Query Match

Best Local Similarity 1.3%; Score 7; DB 2; Length 80;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 LFLNTVR 338

|||||

Db 11 LFLNTVR 17

RESULT 46

C83574

hypothetical protein PA0570 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: C83574

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2003, 08:45:50 ; Search time 17 Seconds
(without alignments)
1496.556 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGAHLVHGWLMLGSL.....DDILMKPSRPMESNPDTG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	363	67.1	550	1 PTH2_HUMAN	P49190 homo sapien
2	33	6.1	546	1 PTH2_RAT	P70555 rattus norv
3	25	4.6	585	1 PTH2_DIDMA	P25107 didelphis m
4	19	3.5	440	1 SCRC_HUMAN	P47872 homo sapien
5	19	3.5	449	1 SCRC_RAT	P23811 rattus norv
6	18	3.3	585	1 PTH2_PIG	P50133 sus scrofa
7	18	3.3	591	1 PTH2_MOUSE	P41593 mus musculu
8	18	3.3	591	1 PTH2_RAT	P25961 rattus norv
9	18	3.3	593	1 PTH2_HUMAN	Q03431 homo sapien
10	16	3.0	445	1 SCRC_RABIT	Q04502 oryctolagus
11	16	3.0	447	1 VIPR_CARAU	Q90308 carassius a
12	13	2.4	455	1 VIPR_RAT	P43219 rattus norv
13	13	2.4	457	1 VIPR_HUMAN	P32241 homo sapien
14	13	2.4	457	1 VIPR_MELGA	Q91085 meleagris g
15	13	2.4	458	1 VIPR_PIG	Q28992 sus scrofa
16	13	2.4	459	1 VIPR_MOUSE	P97751 mus musculu
17	13	2.4	459	1 VIPR_RAT	P30083 rattus norv
18	13	2.4	462	1 VIPR_MESAU	P43218 mesocricetu
19	12	2.2	466	1 VIPR_HUMAN	P48546 homo sapien
20	10	1.8	477	1 GLP1_HUMAN	P47871 homo sapien
21	10	1.8	550	1 GLP2_RAT	Q92040 rattus norv
22	10	1.8	553	1 GLP2_HUMAN	Q95838 homo sapien
23	9	1.7	437	1 VIPS_MOUSE	P41588 mus musculu
24	9	1.7	437	1 VIPS_RAT	P35000 rattus norv
25	9	1.7	438	1 VIPS_HUMAN	P41587 homo sapien
26	9	1.7	463	1 GLP1_HUMAN	P43220 homo sapien
27	9	1.7	463	1 GLP1_RAT	P32301 rattus norv
28	9	1.7	468	1 PACR_HUMAN	P41586 homo sapien
29	9	1.7	485	1 GLR_MOUSE	Q61606 mus musculu
30	9	1.7	485	1 GLR_RAT	P30082 rattus norv
31	9	1.7	489	1 GLP1_MOUSE	O35659 mus musculu
32	9	1.7	496	1 PACR_MOUSE	P70205 mus musculu
33	9	1.7	513	1 PACR_BOVIN	Q29627 bos taurus

RESULT 1

ID	PTH2_HUMAN	STANDARD	PRT	550 AA
AC	P49130			
DT	01-FEB-1996	(Rel. 33, Created)		
DT	01-FEB-1996	(Rel. 33, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DB	Parathyroid hormone receptor precursor (PTH2 receptor).			
GN	PTH2.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID:9606;			
[1]				
RP	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.			
RC	TISSUE=Brain;			
RX	MEDLINE=95318121; PubMed=7797535;			
RA	Usdin T.B., Gruber C., Bonner T.I.;			
RT	"Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor.";			
RL	J. Biol. Chem. 270:15455-15458(1995).			
[2]				
RP	SEQUENCE OF 26-40 AND 306-550 FROM N.A.			
RX	MEDLINE=97079671; PubMed=8921382;			
RA	Usdin T.B., Modi W., Bonner T.I.;			
RT	"Assignment of the human PTH2 receptor gene (PTH2) to chromosome 2q33 by fluorescence in situ hybridization.";			
RL	Genomics 37:140-141(1996).			
CC	-I- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL CYCLASE.			
CC	-I- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.			
CC	-I- ALSO EXPRESSED IN THE TESTIS.			
CC	-I- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; U25128; AAC50157.1; -			
DR	EMBL; U47124; AAA96796.1; -			
DR	EMBL; U47129; AAC50767.1; -			
DR	EMBL; U47125; AAC50767.1; JOINED.			
DR	EMBL; U47126; AAC50767.1; JOINED.			
DR	EMBL; U47127; AAC50767.1; JOINED.			
DR	EMBL; U47128; AAC50767.1; JOINED.			
DR	PIR; A57519; A57519.			
DR	Genew; HGNC:9609; PTHR2.			
DR	MTM; 601469; -			
DR	GO; GO:0005887; C:integral to plasma membrane; TAS			
DR	GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.			
DR	GO; GO:0007186; P:g-protein coupled receptor protein signalin. . .; TAS.			

P32215 rattus norv
P28217 styela plic
Q13324 homo sapien
P47866 rattus norv
P42784 synchococ
O42603 xenopus lae
P35347 mus musculu
P35353 rattus norv
O62772 ovis aries
Q46012 xenopus lae
Q90812 gallus gall
Q60748 mus musculu

DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormu_receptor.
 DR Pfam; PF00002; 7tm.2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR000249; GPCRSECRETIN.
 DR SMART; SM00008; Horm; 1.
 DR PROSITE; PS00649; G PROTEIN RECP F2.1; 1.
 DR PROSITE; PS00650; G PROTEIN RECP F2.2; 1.
 DR PROSITE; PS00227; G PROTEIN RECP F2.3; 1.
 DR PROSITE; PS00261; G PROTEIN RECP F2.4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 546
 FT DOMAIN 27 143
 FT TRANSMEM 144 167
 FT DOMAIN 168 174
 FT TRANSMEM 175 194
 FT DOMAIN 195 235
 FT TRANSMEM 236 258
 FT DOMAIN 259 273
 FT TRANSMEM 274 295
 FT DOMAIN 296 313
 FT TRANSMEM 314 334
 FT DOMAIN 335 361
 FT TRANSMEM 362 380
 FT DOMAIN 381 391
 FT TRANSMEM 392 414
 FT DOMAIN 415 546
 FT CARBOHYD 51 51
 FT CARBOHYD 106 106
 FT CARBOHYD 116 116
 FT CARBOHYD 121 121
 SQ SEQUENCE 550 AA; 62235 MW; 2ADD14DBAG8A9BF8 CRC64;
 Query Match 67.1%; Score 363; DB 1; Length 550;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 LGASLVHGWMLGSCLLARAQLDSGGTITIEQIVLVKAKVQCELNITAIQLQEGNC 63
 DB 4 LGASLVHGWMLGSCLLARAQLDSGGTITIEQIVLVKAKVQCELNITAIQLQEGNC 63
 QY 64 FPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 123
 DB 64 FPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 123
 QY 124 DCLRFLOPDISIGKQFCELYVYVTVGYSISFGSLAVAILIIGYFRRLHCTRYNHML 183
 DB 124 DCLRFLOPDISIGKQFCELYVYVTVGYSISFGSLAVAILIIGYFRRLHCTRYNHML 183
 QY 184 FVSFMLRATSIYFKDVRVHAHIGVKELESIMQDDPQNSIEATSDVKSYIGCKIAYV 243
 DB 184 FVSFMLRATSIYFKDVRVHAHIGVKELESIMQDDPQNSIEATSDVKSYIGCKIAYV 243
 QY 244 IYFLATNYWILVEGYLHNLIFVAFPSDTKYLWGFILGWGPPAFVAAVARATLAD 303
 DB 244 IYFLATNYWILVEGYLHNLIFVAFPSDTKYLWGFILGWGPPAFVAAVARATLAD 303
 QY 304 ARCWELSGADIKIYQAPILAAIGLNFILFLNTRVRLATKIWETNAVGHDTKQYKRLAK 363
 DB 304 ARCWELSGADIKIYQAPILAAIGLNFILFLNTRVRLATKIWETNAVGHDTKQYKRLAK 363
 QY 364 STLVVLVFGVHYIVFVCLPHSTGLGWEIRHMCFLFNSFGFFVSIYICNGEVOAE 423
 DB 364 STLVVLVFGVHYIVFVCLPHSTGLGWEIRHMCFLFNSFGFFVSIYICNGEVOAE 423
 QY 424 VKQWSEKWLNVDMKTPPCGSRGCVLTVTWTHSTSSQSOVAA 467
 DB 424 VKQWSEKWLNVDMKTPPCGSRGCVLTVTWTHSTSSQSOVAA 467
 RESULT 2
 PTH2_RAT

PTH2_RAT STANDARD; PRT; 546 AA.
 P70555;
 01-NOV-1997 (Rel. 35, Created)
 01-NOV-1997 (Rel. 35, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Parathyroid hormone receptor precursor (PTH2 receptor).
 PTHR2.
 Rattus norvegicus (Rat).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=96426194; PubMed=8828488;
 Uesdin T.B., Bonner T.I., Horta G., Mezey E.;
 "Distribution of parathyroid hormone-2 receptor messenger ribonucleic
 acid in rat."; 137:4285-4297(1996).
 Endocrinology 137:4285-4297(1996).
 -1- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE
 ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 ADENYLYL CYCLASE. PTHR2 MAY BE RESPONSIBLE FOR PTH EFFECTS IN A
 NUMBER OF PHYSIOLOGICAL SYSTEMS. IT MAY PLAY A SIGNIFICANT ROLE IN
 PANCREATIC FUNCTION. PTHR2 PRESENCE IN NEURONS INDICATES THAT IT
 MAY FUNCTION AS A NEUROTRANSMITTER RECEPTOR.
 -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN BRAIN, ARTERIAL AND
 CARDIAC ENDOTHELIUM. FOUND AS WELL IN SPERM, IN THE HEAD OF THE
 EPIDIDYMIS. LOWER EXPRESSION IS FOUND IN VASCULAR SMOOTH MUSCLE,
 EXOCRINE PANCREAS, TESTIS AND PLACENTA.
 -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 or send an email to license@isb-sib.ch).
 EMBL; U55836; AAC52849.1;
 InterPro; IPR000832; GPCR secretin.
 InterPro; IPR001879; hormu_receptor.
 Pfam; PF00002; 7tm.2; 1.
 Pfam; PF02793; HRM; 1.
 PRINTS; PR000249; GPCRSECRETIN.
 SMART; SM00008; Horm; 1.
 PROSITE; PS00649; G PROTEIN RECP F2.1; 1.
 PROSITE; PS00650; G PROTEIN RECP F2.2; FALSE_NEG.
 PROSITE; PS00227; G PROTEIN RECP F2.3; 1.
 PROSITE; PS00261; G PROTEIN RECP F2.4; 1.
 G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 SIGNAL 1 24
 CHAIN 25 546
 PARATHYROID HORMONE RECEPTOR.
 DOMAIN 27 143
 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 144 167
 1 (POTENTIAL).
 DOMAIN 168 174
 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 175 194
 2 (POTENTIAL).
 DOMAIN 195 235
 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 236 258
 3 (POTENTIAL).
 DOMAIN 259 273
 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 274 295
 4 (POTENTIAL).
 DOMAIN 296 313
 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 314 334
 5 (POTENTIAL).
 DOMAIN 335 361
 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 362 380
 6 (POTENTIAL).
 DOMAIN 381 391
 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 392 414
 7 (POTENTIAL).
 DOMAIN 415 546
 CYTOPLASMIC (POTENTIAL).
 N-LINKED (GLCNAc...) (POTENTIAL).
 CARBOHYD 51 51
 N-LINKED (GLCNAc...) (POTENTIAL).
 CARBOHYD 106 106
 N-LINKED (GLCNAc...) (POTENTIAL).
 CARBOHYD 116 116
 N-LINKED (GLCNAc...) (POTENTIAL).
 CARBOHYD 121 121
 N-LINKED (GLCNAc...) (POTENTIAL).
 SEQUENCE 546 AA; 61800 MW; 2825AE4040313527 CRC64;

Query Match 6.1%; Score 33; DB 1; Length 546;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YTVGYSIFSGSLAVAILIIGYFRLHCTRNHYH 180
 Db 146 YTVGYSIFSGSLAVAILIIGYFRLHCTRNHYH 178

RESULT 3

PTRR DIDMA STANDARD; PRT; 585 AA.
 AC P25107;
 DT 01-NOV-1992 (Rel. 22, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE precursor (PTH/PTHrP receptor).
 GN PTHR1 OR PTHR.
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 OX NCBI_TaxID=9267;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92054592; PubMed=1658941;
 RA Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Schipani E.,
 RA Richards J., Kolakowski L.F. Jr., Hock J., Potts J.T. Jr.,
 RA Kronenberg H.M., Segre G.V.;
 RT "A G protein-linked receptor for parathyroid hormone and parathyroid
 RT hormone-related peptide.";
 RL Science 254:1024-1026(1991).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
 CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
 CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 CC SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; M74445; AAA30979.1; -;
 CC PIR; A39286; A39286.
 CC HSP; Q03431; IBL1.
 CC InterPro; IPR000832; GPCR_secretin.
 CC InterPro; IPR001879; hormn_receptor.
 CC Pfam; PF00002; 7tm.2; 1.
 CC Pfam; PF02793; Hrm.1.
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; Hormr.1.
 CC PROSITE; PS00649; G PROTEIN RECP F2.1; 1.
 CC PROSITE; PS00650; G PROTEIN RECP F2.2; 1.
 CC PROSITE; PS00227; G PROTEIN RECP F2.3; 1.
 CC PROSITE; PS0261; G PROTEIN RECP F2.4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 KW SIGNAL 1 26
 FT CHAIN 27 585
 FT PARATHYROID HORMONE/ PARATHYROID HORMONE-
 FT RELATED PEPTIDE RECEPTOR.
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 186 209
 FT DOMAIN 210 216
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 217 236
 FT DOMAIN 237 276
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 277 300
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 301 314
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 315 336

FT DOMAIN 337 355
 FT TRANSMEM 356 376
 FT DOMAIN 377 403
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 404 422
 FT DOMAIN 423 434
 FT TRANSMEM 435 457
 FT DOMAIN 458 585
 FT DISULFID 48 114
 FT DISULFID 105 145
 FT DISULFID 128 167
 FT CARBOHYD 148 148
 FT CARBOHYD 158 158
 FT CARBOHYD 163 163
 FT CARBOHYD 173 173
 SQ SEQUENCE 585 AA; 65963 MW; 34900384CD6DF477 CRC64;

Query Match 4.6%; Score 25; DB 1; Length 585;
 Best Local Similarity 100.0%; Pred. No. 2.8e-17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNHYHMLFVFSFMLRA 191

Db 207 GYFRLHCTRNHYHMLFVFSFMLRA 231

RESULT 4

SCRC HUMAN STANDARD; PRT; 440 AA.
 ID SCRC_HUMAN STANDARD; PRT; 440 AA.
 AC P47872; Q12961; Q13213.
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Secretin receptor precursor (SCT-R).
 GN SCTR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Carnivora; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=95169147; PubMed=7864894;
 RA Jiang S., Ulrich C.D.;
 RT "Molecular cloning and functional expression of a human pancreatic
 RT secretin receptor.";
 RL Biochem. Biophys. Res. Commun. 207:883-890(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=95336443; PubMed=7612008;
 RA Chow B.K.-C.;
 RT "Molecular cloning and functional characterization of a human
 RT secretin receptor.";
 RL Biochem. Biophys. Res. Commun. 212:204-211(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=95214632; PubMed=7700244;
 RA Patel D.R., Kong Y., Sreedharan S.P.;
 RT "Molecular cloning and expression of a human secretin receptor.";
 RL Mol. Pharmacol. 47:467-473(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
 CC CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

[illegible]

DR	ENBL; L34610; AAA40011.1; JOINED.
DR	PIR; I59297; I59297.
DR	PIR; S44203; S44203.
DR	HSP; Q03431; 1BL1.
DR	MGI; G7801; Pthr1.
DR	GO; GO:0030282; P.bone mineralization; IMP.
DR	GO; GO:0001501; P.skeletal development; IMP.
DR	InterPro; IPRO00832; GPCR secretin.
DR	InterPro; IPRO01879; hormn_receptor.
DR	Pfam; PF00002; 7tm_2; 1.
DR	Pfam; PF02793; HRM; 1.
DR	PRINTS; PR00249; GPCRSSECRETIN.
DR	SMART; SM00008; Hormr; 1.
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR	PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR	PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT	SIGNAL 1 26
FT	CHAIN 27 591
FT	DOMAIN 27 188
FT	TRANSMEM 189 212
FT	DOMAIN 213 219
FT	TRANSMEM 220 239
FT	DOMAIN 240 282
FT	TRANSMEM 283 306
FT	DOMAIN 307 320
FT	TRANSMEM 321 342
FT	DOMAIN 343 361
FT	TRANSMEM 362 382
FT	DOMAIN 383 409
FT	TRANSMEM 410 428
FT	DOMAIN 429 440
FT	TRANSMEM 441 463
FT	DOMAIN 464 591
FT	DISULFID 48 117
FT	DISULFID 108 148
FT	DISULFID 131 170
QY	245 YFLATNYWILVEGLYLH 262
Db	290 YFLATNYWILVEGLYLH 307
RESULT 8	
PTTR_RAT	ID_PTTR_RAT STANDARD; PRT; 591 AA.
AC	P25961;
DT	01-MAY-1992 (Rel. 22, Created)
DT	01-MAY-1992 (Rel. 22, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Parathyroid hormone/parathyroid hormone-related peptide precursor (PTH/PTHrP receptor).
GN	PTHRI OR PTHRH.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX	NCBI_TaxID=10116;
[1]	
RP	SEQUENCE FROM N.A.
RC	TISSUE=Bone;
RA	MEDLINE=92212903; PubMed=1313566;
RA	Abou-Samra A.-B.; Jueppner H., Force T., Freeman M.W., Kong X.-F., Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr., Kronenberg H.M., Segre G.V.;
RT	"Expression cloning of a common receptor for parathyroid hormone and parathyroid hormone-related peptide from rat osteoblast-like cells: a single receptor stimulates intracellular accumulation of both cAMP and inositol triphosphates and increases intracellular free calcium";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=94292182; PubMed=8020952;
RA	Pausova Z., Bourdon J., Clayton D., Mattei M.-G., Seldin M.F., Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.;
RT	"Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (PTHr) cDNA from a rat osteosarcoma (UMR 106) cell line: genomic assignment of the gene in the human, mouse, and rat genomes.";
RL	Genomics 20:20-26(1994).
CC	-!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATES ADENYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; M77184; AAA41811.1; --
DR	EMBL; L19475; AAA68098.1; --
DR	PIR; I54195; I54195.
DR	HSP; Q03431; 1BL1.
DR	InterPro; IPRO00832; GPCR secretin.
DR	InterPro; IPRO01879; hormn_receptor.
DR	Pfam; PF00002; 7tm_2; 1.
DR	Pfam; PF02793; HRM; 1.
DR	PRINTS; PR00249; GPCRSSECRETIN.
DR	SMART; SM00008; Hormr; 1.
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR	PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR	PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT	SIGNAL 1 26
FT	CHAIN 27 591
FT	DOMAIN 27 188
FT	TRANSMEM 189 212
FT	DOMAIN 213 219
FT	TRANSMEM 220 239
FT	DOMAIN 240 282
FT	TRANSMEM 283 306
FT	DOMAIN 307 320
FT	TRANSMEM 321 342
FT	DOMAIN 343 361
FT	TRANSMEM 362 382
FT	DOMAIN 383 409
FT	TRANSMEM 410 428
FT	DOMAIN 429 440
FT	TRANSMEM 441 463
FT	DOMAIN 464 591
FT	DISULFID 48 117
FT	DISULFID 108 148
FT	DISULFID 131 170
DR	EMBL; M77184; AAA41811.1; --
DR	EMBL; L19475; AAA68098.1; --
DR	PIR; I54195; I54195.
DR	HSP; Q03431; 1BL1.
DR	InterPro; IPRO00832; GPCR secretin.
DR	InterPro; IPRO01879; hormn_receptor.
DR	Pfam; PF00002; 7tm_2; 1.
DR	Pfam; PF02793; HRM; 1.
DR	PRINTS; PR00249; GPCRSSECRETIN.
DR	SMART; SM00008; Hormr; 1.
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR	PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR	PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT	SIGNAL 1 26
FT	CHAIN 27 591
FT	DOMAIN 27 188
FT	TRANSMEM 189 212
FT	DOMAIN 213 219
FT	TRANSMEM 220 239
FT	DOMAIN 240 282
FT	TRANSMEM 283 306
FT	DOMAIN 307 320</

FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 591 AA; 66260 MW; 21944F3051B9E9C1 CRC64;

Query Match 3.3%; Score 18; DB 1; Length 591;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 YFLATNYWILVEGLYIH 262
 DB 290 YFLATNYWILVEGLYIH 307

RESULT 9

PTRR_HUMAN STANDARD; PRT; 593 AA.

AC Q03431;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE Precursor (PTH/PTHrP receptor).
 GN PTHR1 OR PTHR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93238641; PubMed=8386612;
 RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Juppner H.;
 RT "Identical complementary deoxyribonucleic acids encode a human renal
 RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
 RN Endocrinology 132:2157-2165(1993).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93387403; PubMed=8397094;
 RA Schneider H., Feyen J.-H., Rao Movva N.;
 RT "Cloning and functional expression of a human parathyroid hormone
 RT receptor.";
 RL Eur. J. Pharmacol. 246:149-155(1993).
 RL [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95263723; PubMed=7745008;
 RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,
 RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidke J., Dop C.,
 RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Juppner H.;
 RT "Pseudohypoparathyroidism type Ib is not caused by mutations in the
 RT coding exons of the human parathyroid hormone (PTH)/PTH-related
 RT peptide receptor gene.";
 RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).
 RL [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Levine M.A.;
 RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP EXTRACELLULAR DOMAIN DISULFIDE BONDS.
 RX MEDLINE=20374569; PubMed=10913300;
 RA Grauschopf U., Lillie H., Honold K., Wozny M., Reusch D., Esswein A.,
 RA Schaefer W., Rucknagel K.P., Rudolph R.;
 RT "The N-terminal fragment of human parathyroid hormone receptor 1
 RT constitutes a hormone binding domain and reveals a distinct disulfide
 RT pattern.";
 RL Biochemistry 39:8878-8887(2000).
 RN [6]
 RP STRUCTURE BY NMR OF 168-198.

RX MEDLINE=98409436; PubMed=9737850;
 RA Pellegrini M., Bisello A., Rosenblatt M., Choev M., Mierke D.F.;
 RT "Binding domain of human parathyroid hormone receptor: from
 RT conformation to function.";
 RL Biochemistry 37:12737-12743(1998).
 RN [7]
 RP VARIANT MURK-JANSEN ARG-223.
 RX MEDLINE=95215874; PubMed=7701349;
 RA Schipani E., Kruse K., Juppner H.;
 RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type
 RT metaphyseal chondrodysplasia.";
 RL Science 268:98-100(1995).
 RN [8]
 RP VARIANTS MURK-JANSEN ARG-223 AND PRO-410.
 RX MEDLINE=96366745; PubMed=8703170;
 RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
 RA Kooh S.W., Cole W.G., Juppner H.;
 RT "Constitutively activated receptors for parathyroid hormone and
 RT parathyroid hormone-related peptide in Jansen's metaphyseal
 RT chondrodysplasia.";
 RL New Engl. J. Med. 335:708-714(1996).
 RN [9]
 RP MUTAGENESIS OF ARG-223 AND PRO-410.
 RX MEDLINE=97322091; PubMed=9178745;
 RA Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
 RA Juppner H.;
 RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
 RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
 RT receptors mutated at the two loci for Jansen's metaphyseal
 RT chondrodysplasia.";
 RL Mol. Endocrinol. 11:851-858(1997).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
 CC RECEPTOR HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 CC SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN
 CC KIDNEY, BONE AND LIVER.
 CC -1- DISEASE: DEFECTS IN PTHR1 ARE THE CAUSE OF BLOOMSTRAND TYPE OF
 CC CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA.
 CC -1- DISEASE: DEFECTS IN PTHR1 ARE THE CAUSE OF MURK-JANSEN TYPE OF
 CC METAPHYSEAL CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA. IT IS
 CC A RARE FORM OF SHORT-LIMBED DWARFISM ASSOCIATED WITH HYPERCALCEMIA
 CC AND NORMAL OR LOW SERUM CONCENTRATIONS OF THE TWO PARATHYROID
 CC HORMONES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).

DR EMBL; L04308; AAA3525.1; --
 DR EMBL; X68596; CAA48589.1; --
 DR EMBL; U22401; AAB60657.1; --
 DR EMBL; U22401; AAB60657.1; JOINED.
 DR EMBL; U22402; AAB60657.1; JOINED.
 DR EMBL; U22403; AAB60657.1; JOINED.
 DR EMBL; U22404; AAB60657.1; JOINED.
 DR EMBL; U22405; AAB60657.1; JOINED.
 DR EMBL; U22406; AAB60657.1; JOINED.
 DR EMBL; U22407; AAB60657.1; JOINED.
 DR EMBL; U22408; AAB60657.1; JOINED.
 DR EMBL; U17418; AAA56774.1; --
 DR PIR; I38139; A49191.
 DR PDB; 1BL1; 30-MAR-99.
 DR PDB; 1ET2; 06-SEP-00.
 DR PDB; 1ET3; 06-SEP-00.
 DR Genew; HGNC:9608; PTHR1.

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DR MIM; 168468; --
DR MIM; 156400; --
DR MIM; 215045; --
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0004991; F:parathyroid hormone receptor activity; TAS.
DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G PROTEIN RECP_F2_1; 1.
DR PROSITE; PS00650; G PROTEIN RECP_F2_2; 1.
DR PROSITE; PS02227; G PROTEIN RECP_F2_3; 1.
DR PROSITE; PS0261; G PROTEIN RECP_F2_4; 1.
DR PROSITE; PS0261; G PROTEIN RECP_F2_4; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
DR Disease mutation; 3D-structure; Dwarfism.
FT SIGNAL 1 26
FT CHAIN 27 593
FT PARATHYROID HORMONE/PARATHYROID HORMONE-
FT RELATED PEPTIDE RECEPTOR.
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 27 188
FT TRANSMEM 189 212
FT DOMAIN 213 219
FT TRANSMEM 220 239
FT DOMAIN 240 282
FT TRANSMEM 283 306
FT DOMAIN 307 320
FT TRANSMEM 321 342
FT DOMAIN 343 361
FT TRANSMEM 362 382
FT DOMAIN 383 409
FT TRANSMEM 410 428
FT DOMAIN 429 440
FT TRANSMEM 441 463
FT DOMAIN 464 593
FT DISULFID 48 117
FT DISULFID 108 148
FT DISULFID 131 170
FT CARBOHYD 151 151
FT CARBOHYD 161 161
FT CARBOHYD 166 166
FT CARBOHYD 176 176
FT VARIANT 223 223
FT VARIANT 410 410
FT CONFLICT 471 471
FT CONFLICT 473 473
FT HELIX 169 176
FT HELIX 180 185
FT HELIX 188 196
FT SEQUENCE 593 AA; 66360 MW; DAL400640A6C7F2B CRC64;
Query Match 3.3%; Score 18; DB 1; Length 593;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 YFLATNYWLVGLYH 262
| | | | | | | | | | | | | | | | | |
Db 290 YFLATNYWLVGLYH 307
| | | | | | | | | | | | | | | | | |
RESULT 10
SCRC RABIT
ID SCRC RABIT STANDARD; PRT; 445 AA.
AC O46502;
DT 15-JUL-1999 (Rel. 38, Created)

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DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Secretin receptor precursor (SCT-R).
GN SCTR
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98366112; PubMed=9700755;
RA Svoboda M., Tastednoy M., de Neef P., Delporte C., Waelbroeck M.,
RA Robberecht P.;
RT "Molecular cloning and in vitro properties of the recombinant rabbit
RT secretin receptor.";
RL Peptides 19:1055-1062(1998).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF025411; AAC32767.1; --
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G PROTEIN RECP_F2_1; 1.
DR PROSITE; PS00650; G PROTEIN RECP_F2_2; 1.
DR PROSITE; PS02227; G PROTEIN RECP_F2_3; 1.
DR PROSITE; PS0261; G PROTEIN RECP_F2_4; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 445
FT SECRETIN RECEPTOR.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 140 163
FT DOMAIN 164 170
FT TRANSMEM 171 190
FT DOMAIN 191 212
FT TRANSMEM 213 236
FT DOMAIN 237 250
FT TRANSMEM 251 272
FT DOMAIN 273 290
FT TRANSMEM 291 313
FT DOMAIN 314 339
FT TRANSMEM 340 358
FT DOMAIN 359 365
FT TRANSMEM 366 388
FT DOMAIN 389 445
FT CARBOHYD 68 68
FT CARBOHYD 96 96
FT CARBOHYD 102 102
FT CARBOHYD 124 124
FT SEQUENCE 445 AA; 50495 MW; 31C4169CB099F194 CRC64;
Query Match 3.0%; Score 16; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 FRRLHCTRNVIHMLF 184
| | | | | | | | | | | | | | | | | |
Db 163 FRRLHCTRNVIHMLF 178
| | | | | | | | | | | | | | | | | |

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RESULT 11
VIPR_CARAU STANDARD; PRT; 447 AA.
AC Q90308;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vasoactive intestinal polypeptide receptor (VIP-R) (VIP receptor).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190233; PubMed=9038250;
RA Chow B.K.C., Yuen T.T.H., Chan K.W.;
RT "Molecular evolution of vertebrate VIP receptors and functional
characterization of a VIP receptor from goldfish Carassius auratus.";
RL Gen. Comp. Endocrinol. 105:176-185(1997).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; U56391; AB05459.1; -.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 128 1 (POTENTIAL).
FT DOMAIN 129 135 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 136 155 2 (POTENTIAL).
FT DOMAIN 156 178 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 179 202 3 (POTENTIAL).
FT DOMAIN 203 216 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 217 238 4 (POTENTIAL).
FT DOMAIN 239 256 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 257 280 5 (POTENTIAL).
FT DOMAIN 281 305 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 306 325 6 (POTENTIAL).
FT DOMAIN 326 337 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 338 357 7 (POTENTIAL).
FT DOMAIN 358 447 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 177 247 BY SIMILARITY.
FT CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 447 AA; 50959 MW; 66839E243702554C CRC64;
Query Match 3.0%; Score 16; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 172 LHCTRYNHMLFVSP 187
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Db 131 LHCTRYNHMLFVSP 146

RESULT 12
GIPR_RAT STANDARD; PRT; 455 AA.
AC P43219;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gastric inhibitory polypeptide receptor precursor (GIP-R) (Glucose-
dependent insulinotropic polypeptide receptor).
GN GIPR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=94062667; PubMed=8243312;
RA Usdin T.B., Mezey E., Button D.C., Brownstein M.J., Bonner T.I.;
RT "Gastric inhibitory polypeptide receptor, a member of the secretin-
vasoactive intestinal peptide receptor family, is widely distributed
in peripheral organs and the brain.";
RL Endocrinology 133:2861-2871(1993).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: PRESENT IN THE PANCREAS AS WELL AS THE GUT.
ADIPOSE TISSUE, HEART, PITUITARY, AND INNER LAYERS OF THE ADRENAL
CORTEX, WHEREAS IT IS NOT FOUND IN KIDNEY, SPLEEN, OR LIVER. IT IS
ALSO EXPRESSED IN SEVERAL BRAIN REGIONS, INCLUDING THE CEREBRAL
CORTEX, HIPPOCAMPUS, AND OLFACTORY BULB.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; L19660; AAC37637.1; -.
CC PIR; I53273; I53273.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT CHAIN 1 18 POTENTIAL.
FT DOMAIN 19 455 GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.
FT TRANSMEM 19 135 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 136 158 1 (POTENTIAL).
FT TRANSMEM 159 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 186 2 (POTENTIAL).
FT DOMAIN 187 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 239 3 (POTENTIAL).
FT DOMAIN 240 251 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 252 275 4 (POTENTIAL).
FT DOMAIN 276 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 291 316 5 (POTENTIAL).

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FT DOMAIN 317 338 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 339 359 6 (POTENTIAL).
 FT DOMAIN 360 374 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 375 395 7 (POTENTIAL).
 FT DOMAIN 396 455 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 59 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 455 AA; 52256 MW; 5454B0638ABF9A06 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNVIHM 181
 DB 159 FRRLHCTRNVIHM 171
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RESULT 13
 VIPR_HUMAN STANDARD; PRT; 457 AA.
 AC P32241; Q15871;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1)
 DE (Pituitary adenylate cyclase activating polypeptide type II receptor)
 DE (PACAP type II receptor) (PACAP-R-2).
 GN VIPR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=93290641; PubMed=8390245;
 RA Sreedharan S.P., Patel D.R., Huang J.-X., Goetzl E.J.;
 RT "Cloning and functional expression of a human neuroendocrine
 RT vasoactive intestinal peptide receptor.";
 RL Biochem. Biophys. Res. Commun. 193:546-553(1993).
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Intestine;
 RX MEDLINE=942335025; PubMed=8179610;
 RA Couvineau A., Rouyer-Fessard C., Darmoul D., Maoret J.J., Carrero I.,
 RA Ogier-Denis E., Laburthe M.;
 RT "Human intestinal VIP receptor: cloning and functional expression of
 RT two cDNA encoding proteins with different N-terminal domains.";
 RL Biochem. Biophys. Res. Commun. 200:769-776(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 33-457 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=95001220; PubMed=7917790;
 RA Gagnon A.W., Aiyar N., Elshourbagy N.A.;
 RT "Molecular cloning and functional characterization of a human liver
 RT vasoactive intestinal peptide receptor.";
 RL Cell. Signal. 6:321-333(1994).
 RN [5]
 RP DISULFIDE BOND.
 RX MEDLINE=99126981; PubMed=9928020;
 RA Knudsen S.M., Tams J.W., Wulff B.S., Fahrenkrug J.;
 RT "Importance of conserved cysteines in the extracellular loops of
 RT human PACAP/VIP1 receptor for ligand binding and stimulation of cAMP
 RT production.";

Ann. N.Y. Acad. Sci. 865:259-265(1998).
 -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
 RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
 CYCLASE. THE AFFINITY IS VIP = PACAP-27 > PACAP-38.
 -!- SUBCELLULAR LOCATION: Integral membrane protein.
 -!- ALTERNATIVE PRODUCTS;
 Event=Alternative splicing; Named isoforms=2;
 Name=Short; Synonyms=hIVR8;
 IsoId=P32241-1; Sequence=Displayed;
 Name=Long; Synonyms=hIVR5;
 IsoId=P32241-2; Sequence=VSP 002010;
 -!- TISSUE SPECIFICITY: IN LUNG, HT29 COLONIC EPITHELIAL CELLS, RAJI
 B-LYMPHOBLASTS. LESSER EXTENT IN BRAIN, HEART, KIDNEY, LIVER AND
 PLACENTA.
 -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

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 EMBL; U11087; AAB60362.1; -;
 EMBL; U11079; AAB60362.1; JOINED.
 EMBL; U11080; AAB60362.1; JOINED.
 EMBL; U11081; AAB60362.1; JOINED.
 EMBL; U11083; AAB60362.1; JOINED.
 EMBL; U11084; AAB60362.1; JOINED.
 EMBL; U11085; AAB60362.1; JOINED.
 EMBL; U11086; AAB60362.1; JOINED.
 EMBL; U13288; AAA36805.1; -;
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 EMBL; X75299; CAA53046.1; -;
 EMBL; AB056669; BAC05895.1; -;
 EMBL; L20295; AAA36802.1; -;
 PIR; JC2194; JC2194.
 DR Genew; HGNC:12694; VIPR1.
 DR MIM; 192321; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004999; F:vasoactive intestinal polypeptide receptor . . .; TAS.
 DR GO; GO:0007586; P:digestion; TAS.
 DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR GO; GO:0006936; P:muscle contraction; TAS.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 DR GO; GO:0007268; P:synaptic transmission; TAS.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
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 DR PROSITE; PS00835; G-PROTEIN RECP F2_187; 1.
 DR PROSITE; PS00836; G-PROTEIN RECP F2_188; 1.
 DR PROSITE; PS00837; G-PROTEIN RECP F2_189; 1.
 DR PROSITE; PS00838; G-PROTEIN RECP F2_190; 1.
 DR PROSITE; PS00839; G-PROTEIN RECP F2_191; 1.
 DR PROSITE; PS00840; G-PROTEIN RECP F2_192; 1.
 DR PROSITE; PS00841; G-PROTEIN RECP F2_193; 1.
 DR PROSITE; PS00842; G-PROTEIN RECP F2_194; 1.
 DR PROSITE; PS00843; G-PROTEIN RECP F2_195; 1.
 DR PROSITE; PS00844; G-PROTEIN RECP F2_196; 1.
 DR PROSITE; PS00845; G-PROTEIN RECP F2_197; 1.
 DR PROSITE; PS00846; G-PROTEIN RECP F2_198; 1.
 DR PROSITE; PS00847; G-PROTEIN RECP F2_199; 1.
 DR PROSITE; PS00848; G-PROTEIN RECP F2_200; 1.
 DR PROSITE; PS00849; G-PROTEIN RECP F2_201; 1.
 DR PROSITE; PS00850; G-PROTEIN RECP F2_202; 1.
 DR PROSITE; PS00851; G-PROTEIN RECP F2_203; 1.
 DR PROSITE; PS00852; G-PROTEIN RECP F2_204; 1.
 DR PROSITE; PS00853; G-PROTEIN RECP F2_205; 1.
 DR PROSITE; PS00854; G-PROTEIN RECP F2_206; 1.
 DR PROSITE; PS00855; G-PROTEIN RECP F2_207; 1.
 DR PROSITE; PS00856; G-PROTEIN RECP F2_208; 1.
 DR PROSITE; PS00857; G-PROTEIN RECP F2_209; 1.
 DR PROSITE; PS00858; G-PROTEIN RECP F2_210; 1.
 DR PROSITE; PS00859; G-PROTEIN RECP F2_211; 1.
 DR PROSITE; PS00860; G-PROTEIN RECP F2_212; 1.
 DR PROSITE; PS00861; G-PROTEIN RECP F2_213; 1.
 DR PROSITE; PS00862; G-PROTEIN RECP F2_214; 1.
 DR PROSITE; PS00863; G-PROTEIN RECP F2_215; 1.
 DR PROSITE; PS00864; G-PROTEIN RECP F2_216; 1.
 DR PROSITE; PS00865; G-PROTEIN RECP F2_217; 1.
 DR PROSITE; PS00866; G-PROTEIN RECP F2_218; 1.
 DR PROSITE; PS00867; G-PROTEIN RECP F2_219; 1.
 DR PROSITE; PS00868; G-PROTEIN RECP F2_220; 1.
 DR PROSITE; PS00869; G-PROTEIN RECP F2_221; 1.
 DR PROSITE; PS00870; G-PROTEIN RECP F2_222; 1.
 DR PROSITE; PS00871; G-PROTEIN RECP F2_223; 1.
 DR PROSITE; PS00872; G-PROTEIN RECP F2_224; 1.
 DR PROSITE; PS00873; G-PROTEIN RECP F2_225; 1.
 DR PROSITE; PS00874; G-PROTEIN RECP F2_226; 1.
 DR PROSITE; PS00875; G-PROTEIN RECP F2_227; 1.
 DR PROSITE; PS00876; G-PROTEIN RECP F2_228; 1.
 DR PROSITE; PS00877; G-PROTEIN RECP F2_229; 1.
 DR PROSITE; PS00878; G-PROTEIN RECP F2_230; 1.
 DR PROSITE; PS00879; G-PROTEIN RECP F2_231; 1.
 DR PROSITE; PS00880; G-PROTEIN RECP F2_232; 1.
 DR PROSITE; PS00881; G-PROTEIN RECP F2_233; 1.
 DR PROSITE; PS00882; G-PROTEIN RECP F2_234; 1.
 DR PROSITE; PS00883; G-PROTEIN RECP F2_235; 1.
 DR PROSITE; PS00884; G-PROTEIN RECP F2_236; 1.
 DR PROSITE; PS00885; G-PROTEIN RECP F2_237; 1.
 DR PROSITE; PS00886; G-PROTEIN RECP F2_238; 1.
 DR PROSITE; PS00887; G-PROTEIN RECP F2_239; 1.
 DR PROSITE; PS00888; G-PROTEIN RECP F2_240; 1.
 DR PROSITE; PS00889; G-PROTEIN RECP F2_241; 1.
 DR PROSITE; PS00890; G-PROTEIN RECP F2_242; 1.
 DR PROSITE; PS00891; G-PROTEIN RECP F2_243; 1.
 DR PROSITE; PS00892; G-PROTEIN RECP F2_244; 1.
 DR PROSITE; PS00893; G-PROTEIN RECP F2_245; 1.
 DR PROSITE; PS00894; G-PROTEIN RECP F2_246; 1.
 DR PROSITE; PS00895; G-PROTEIN RECP F2_247; 1.
 DR PROSITE; PS00896; G-PROTEIN RECP F2_248; 1.
 DR PROSITE; PS00897; G-PROTEIN RECP F2_249; 1.
 DR PROSITE; PS00898; G-PROTEIN RECP F2_250; 1.
 DR PROSITE; PS00899; G-PROTEIN RECP F2_251; 1.
 DR PROSITE; PS00900; G-PROTEIN RECP F2_252; 1.
 DR PROSITE; PS00901; G-PROTEIN RECP F2_253; 1.
 DR PROSITE; PS00902; G-PROTEIN RECP F2_254; 1.
 DR PROSITE; PS00903; G-PROTEIN RECP F2_255; 1.
 DR PROSITE; PS00904; G-PROTEIN RECP F2_256; 1.
 DR PROSITE; PS00905; G-PROTEIN RECP F2_257; 1.
 DR PROSITE; PS00906; G-PROTEIN RECP F2_258; 1.
 DR PROSITE; PS00907; G-PROTEIN RECP F2_259; 1.
 DR PROSITE; PS00908; G-PROTEIN RECP F2_260; 1.
 DR PROSITE; PS00909; G-PROTEIN RECP F2_261; 1.
 DR PROSITE; PS00910; G-PROTEIN RECP F2_262; 1.
 DR PROSITE; PS00911; G-PROTEIN RECP F2_263; 1.
 DR PROSITE; PS00912; G-PROTEIN RECP F2_264; 1.
 DR PROSITE; PS00913; G-PROTEIN RECP F2_265; 1.
 DR PROSITE; PS00914; G-PROTEIN RECP F2_266; 1.
 DR PROSITE; PS00915; G-PROTEIN RECP F2_267; 1.
 DR PROSITE; PS00916; G-PROTEIN RECP F2_268; 1.
 DR PROSITE; PS00917; G-PROTEIN RECP F2_269; 1.
 DR PROSITE; PS00918; G-PROTEIN RECP F2_270; 1.
 DR PROSITE; PS00919; G-PROTEIN RECP F2_271; 1.
 DR PROSITE; PS00920; G-PROTEIN RECP F2_272; 1.
 DR PROSITE; PS00921; G-PROTEIN RECP F2_273; 1.
 DR PROSITE; PS00922; G-PROTEIN RECP F2_274; 1.
 DR PROSITE; PS00923; G-PROTEIN RECP F2_275; 1.
 DR PROSITE; PS00924; G-PROTEIN RECP F2_276; 1.
 DR PROSITE; PS00925; G-PROTEIN RECP F2_277; 1.
 DR PROSITE; PS00926; G-PROTEIN RECP F2_278; 1.
 DR PROSITE; PS00927; G-PROTEIN RECP F2_279; 1.
 DR PROSITE; PS00928; G-PROTEIN RECP F2_280; 1.
 DR PROSITE; PS00929; G-PROTEIN RECP F2_281; 1.
 DR PROSITE; PS00930; G-PROTEIN RECP F2_282; 1.
 DR PROSITE; PS00931; G-PROTEIN RECP F2_283; 1.
 DR PROSITE; PS00932; G-PROTEIN RECP F2_284; 1.
 DR PROSITE; PS00933; G-PROTEIN RECP F2_285; 1.
 DR PROSITE; PS00934; G-PROTEIN RECP F2_286; 1.
 DR PROSITE; PS00935; G-PROTEIN RECP F2_287; 1.
 DR PROSITE; PS00936; G-PROTEIN RECP F2_288; 1.
 DR PROSITE; PS00937; G-PROTEIN RECP F2_289; 1.
 DR PROSITE; PS00938; G-PROTEIN RECP F2_290; 1.
 DR PROSITE; PS00939; G-PROTEIN RECP F2_291; 1.
 DR PROSITE; PS00940; G-PROTEIN RECP F2_292; 1.
 DR PROSITE; PS00941; G-PROTEIN RECP F2_293; 1.
 DR PROSITE; PS00942; G-PROTEIN RECP F2_294; 1.
 DR PROSITE; PS00943; G-PROTEIN RECP F2_295; 1.
 DR PROSITE; PS00944; G-PROTEIN RECP F2_296; 1.
 DR PROSITE; PS00945; G-PROTEIN RECP F2_297; 1.
 DR PROSITE; PS00946; G-PROTEIN RECP F2_298; 1.
 DR PROSITE; PS00947; G-PROTEIN RECP F2_299; 1.
 DR PROSITE; PS00948; G-PROTEIN RECP F2_300; 1.
 DR PROSITE; PS00949; G

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FT DOMAIN 317 341 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 342 361 6 (POTENTIAL).
FT DOMAIN 362 373 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 374 393 7 (POTENTIAL).
FT DOMAIN 394 457 CYTOPLASMIC (POTENTIAL).
FT DISULFID 215 285 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 58 69 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 69 69 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 1 32 MPPSPPLPARMLCVLAGALWAGPAGQAA -> MPPPPP
LGLRLGLGWSAVTLVVAAGARSGRGRCGAGGGR
GGVARRRLLELAABSLGSS (in isoform Long).
/FTID=VSP_002010.
G -> GLLR (IN REF. 2).
FT CONFLICT 284 284
FT SEQUENCE 457 AA; 51547 MW; DAA40CF5BEC47D7D CRC64;
Query Match 2.4%; Score 13; DB 1; Length 457;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 172 LHCTNRYIHMLF 184
Db 170 LHCTNRYIHMLF 182
RESULT 14
VIPR MELGA
AC Q91085; STANDARD; PRT; 457 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vasoactive intestinal polypeptide receptor precursor (VIP-R) (VIP
DE receptor).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND
RP INDUCTION.
RC TISSUE=Pituitary, and Small intestine;
RX MEDLINE=21560659; PubMed=11703071;
RA You S., Hsu C.-C., Kim H., Kho Y., Choi Y.J., el Halawani M.E.,
RA Farris J., Foster D.N.;
RT "Molecular cloning and expression analysis of the turkey vasoactive
RT intestinal peptide receptor.";
RL Gen. Comp. Endocrinol. 124:53-65(2001).
RN [2]
RP SEQUENCE OF 198-457 FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96206340; PubMed=8618952;
RA Xu M., Proudman J.A., Pitts G.R., Wong E.A., Foster D.N.,
RA el Halawani M.E.;
RT "Vasoactive intestinal peptide stimulates prolactin mRNA expression
RT in turkey pituitary cells: effects of dopaminergic drugs.";
RL Proc. Soc. Exp. Biol. Med. 212:52-62(1996).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in pituitary, hypothalamus, small
CC intestine and ovarian follicles.
CC -!- DEVELOPMENTAL STAGE: Pituitary levels are highest in
CC nonphotostimulated and incubating birds and lower in
CC photostimulated, laying and photorefractory birds.
CC -!- INDUCTION: Pituitary levels decrease on VIP immunization.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U31991; AAA99740.2; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; HORMR; 1.
DR PROSITE; PS00649; G-PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G-PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02227; G-PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS02261; G-PROTEIN_RECEP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 457 VASOACTIVE INTESTINAL POLYPEPTIDE
RECEPTOR.
FT DOMAIN 20 141 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 142 166 1 (POTENTIAL).
FT DOMAIN 167 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 193 2 (POTENTIAL).
FT DOMAIN 194 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 239 3 (POTENTIAL).
FT DOMAIN 240 253 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 254 275 4 (POTENTIAL).
FT DOMAIN 276 292 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 293 316 5 (POTENTIAL).
FT DOMAIN 317 341 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 342 361 6 (POTENTIAL).
FT DOMAIN 362 373 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 374 393 7 (POTENTIAL).
FT DOMAIN 394 457 CYTOPLASMIC (POTENTIAL).
FT DISULFID 214 284 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 457 AA; 52769 MW; D862F1F2BE4ECB8C CRC64;
Query Match 2.4%; Score 13; DB 1; Length 457;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 172 LHCTNRYIHMLF 184
Db 169 LHCTNRYIHMLF 181
RESULT 15
VIPR_PIG
ID VIPR_PIG STANDARD; PRT; 458 AA.
AC Q28992;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1)
DE (Pituitary adenylate cyclase activating polypeptide type II receptor)
DE (PACAP type II receptor) (PACAP-R-2).
GN VIPR1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RA Hsiung H.M., Smith D.P., Hyslop P.A., Heiman M.L., Hassan H.A.,
RA Zhang X.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL

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FT DOMAIN 364 375 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 376 395 7 (POTENTIAL).
 FT DOMAIN 396 459 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 216 286 BY SIMILARITY.
 FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 459 AA; 52094 MW; C0C3A9AELADF611D CRC64;

 Query Match 2.4%; Score 13; DB 1; Length 459;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 172 LHCTRNHYHMLF 184
 DB 171 LHCTRNHYHMLF 183

 RESULT 17
 VIPR_RAT
 ID VIPR_RAT STANDARD; PRT; 459 AA.
 AC P30083;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1)
 DE (Pituitary adenylate cyclase activating polypeptide type II receptor)
 DE (PACAP type II receptor) (PACAP-R-2).
 GN VIPR1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=922332309; PubMed=1314625;
 RA Ishihara T., Shigemoto R., Mori K., Takahashi K., Nagata S.;
 RT "Functional expression and tissue distribution of a novel receptor
 RT for vasoactive intestinal polypeptide.";
 RL Neuron 8:811-819(1992).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CC CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: IN LIVER, LUNG, INTESTINES, THYMUS AND BRAIN
 CC (MOSTLY IN THE CEREBRAL CORTEX AND HIPPOCAMPUS).
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL; M86835; AAA42331.1; -.
 DR PIR; JH0594; JH0594.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PF00249; GPCRSSECRETIN.
 DR SMART; SM00086; Hormk; 1.
 DR PROSITE; PS00649; G-PROTEIN RECEPTOR_F2_1; 1.
 DR PROSITE; PS00650; G-PROTEIN RECEPTOR_F2_2; 1.
 DR PROSITE; PS50227; G-PROTEIN RECEPTOR_F2_3; 1.
 DR PROSITE; PS50261; G-PROTEIN RECEPTOR_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 30 POTENTIAL.

FT CHAIN 31 459 VASOACTIVE INTESTINAL POLYPEPTIDE
 FT RECEPTOR 1.
 FT EXTRACELLULAR (POTENTIAL).
 FT 1 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 2 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 3 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 4 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 5 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 6 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 7 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT BY SIMILARITY.
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 459 AA; 52057 MW; 99E8957DA86698D2 CRC64;

 Query Match 2.4%; Score 13; DB 1; Length 459;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 172 LHCTRNHYHMLF 184
 DB 171 LHCTRNHYHMLF 183

 RESULT 18
 GIPR_MESAU
 ID GIPR_MESAU STANDARD; PRT; 462 AA.
 AC P43218;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Gastric inhibitory polypeptide receptor precursor (GIP-R) (Glucose-
 DE dependent insulinotropic polypeptide receptor).
 GN GIPR.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95110292; PubMed=7811236;
 RA Yasuda K., Inagaki N., Yamada Y., Kubota A., Seino S., Seino Y.;
 RT "Hamster gastric inhibitory polypeptide receptor expressed in
 RT pancreatic islets and clonal insulin-secreting cells: its structure
 RT and functional properties.";
 RL Biochem. Biophys. Res. Commun. 205:1556-1562(1994).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CC CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED INCLUDING PANCREATIC
 CC ISLETS, BRAIN AND VARIOUS PERIPHERAL TISSUES.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL; D38103; BAA07284.1; -.
 DR

DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G-PROTEIN RECP_F2_1; 1.
 DR PROSITE; PS00650; G-PROTEIN RECP_F2_2; 1.
 DR PROSITE; PS00227; G-PROTEIN RECP_F2_3; 1.
 DR PROSITE; PS00261; G-PROTEIN RECP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 462 GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.
 FT DOMAIN 19 135 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 136 158 1 (POTENTIAL).
 FT DOMAIN 159 166 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 167 186 2 (POTENTIAL).
 FT DOMAIN 187 214 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 215 239 3 (POTENTIAL).
 FT DOMAIN 240 251 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 252 275 4 (POTENTIAL).
 FT DOMAIN 276 290 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 291 316 5 (POTENTIAL).
 FT DOMAIN 317 338 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 339 359 6 (POTENTIAL).
 FT DOMAIN 360 374 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 375 395 7 (POTENTIAL).
 FT DOMAIN 396 462 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 462 AA; 52918 MW; D7A6204BCB9B88 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 462;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYNIHM 181
 |||||
 Db 159 FRLHCTRYNIHM 171

RESULT 19
 GIPR_HUMAN STANDARD; PRT; 466 AA.
 AC P48546; Q14401; Q16400;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gastric inhibitory polypeptide receptor precursor (GIP-R) (Glucose-dependent insulinotropic polypeptide receptor).
 GN GIPR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RA Usdin T.B., Gruber C., Modi W., Bonner T.I.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RX MEDLINE=96013879; PubMed=7589426;
 RA Volz A., Goke R., Lankat-Buttgereit B., Fehmann H.C., Bode H.P.,
 RA Goke B.;
 RT "Molecular cloning, functional expression, and signal transduction of the GIP-receptor cloned from a human insulinoma."
 RL FEBS Lett. 373:23-29(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC TISSUE=Pancreas;
 RX MEDLINE=96007224; PubMed=7556958;
 RA Gremlich S., Porret A., Hani E.H., Cherif D., Vionnet N., Froguel P.,
 RA Thorens B.;

RT "Cloning, functional expression, and chromosomal localization of the human pancreatic islet glucose-dependent insulinotropic polypeptide receptor."
 RL Diabetes 44:1202-1208(1995).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RX MEDLINE=96121393; PubMed=8575774;
 RA Yamada Y., Hayami T., Nakamura K., Kaisaki P.J., Someya Y.,
 RA Wang C.Z., Seino S., Seino Y.;
 RT "Human gastric inhibitory polypeptide receptor: cloning of the gene (GIPR) and cDNA."
 RL Genomics 29:773-776(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
 RA Danganan L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of a 1.9 Mb region in 19q13.2 between APOE and D19S412."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Short;
 CC IsoID=P48546-1; Sequence=Displayed;
 CC Name=Long;
 CC IsoID=P48546-2; Sequence=VSP_002002;
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL; U39231; A384418.1; -
 CC EMBL; S79852; A385419.2; -
 CC EMBL; X81832; CAA57426.1; -
 CC EMBL; D49559; BAA08503.1; -
 CC EMBL; D49556; BAA08503.1; JOINED.
 CC EMBL; D49557; BAA08503.1; JOINED.
 CC EMBL; D49558; BAA08503.1; JOINED.
 CC EMBL; AC006132; AAC97984.1; -
 CC FIR; G02234; G02234.
 CC FIR; S66676; S66676.
 CC Genew; HGNC:4271; GIPR.
 CC MIM; 137241; -
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0007190; P:adenylate cyclase activation; TAS.
 CC GO; GO:0006091; P:energy pathways; TAS.
 CC GO; GO:0007584; P:nutritional response pathway; TAS.
 CC InterPro; IPR000832; GPCR_secretin.
 CC InterPro; IPR001879; hormn_receptor.
 CC Pfam; PF00002; 7tm_2; 1.
 CC Pfam; PF02793; HRM; 1.
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; Hormr; 1.
 CC PROSITE; PS00649; G-PROTEIN RECP_F2_1; 1.
 CC PROSITE; PS00650; G-PROTEIN RECP_F2_2; 1.
 CC PROSITE; PS00227; G-PROTEIN RECP_F2_3; 1.
 CC PROSITE; PS00261; G-PROTEIN RECP_F2_4; 1.
 CC PROSITE; PS00261; G-PROTEIN RECP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;

KW Alternative splicing; Polymorphism.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 466 GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.
 FT DOMAIN 22 138 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 139 161 1 (POTENTIAL).
 FT DOMAIN 162 169 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 170 189 2 (POTENTIAL).
 FT DOMAIN 190 217 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 218 242 3 (POTENTIAL).
 FT DOMAIN 243 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 278 4 (POTENTIAL).
 FT DOMAIN 279 293 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 294 319 5 (POTENTIAL).
 FT DOMAIN 320 341 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 342 362 6 (POTENTIAL).
 FT DOMAIN 363 377 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 378 398 7 (POTENTIAL).
 FT DOMAIN 399 466 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 77 77 V -> VGRDPAAPALWRRRTAPPLSAIVSQV (in isoform Long).
 FT VARSPLIC 399 399 /FTid=VSP_002002.
 FT VARIANT 207 207 A -> V (IN dbSNP:1800436).
 FT VARIANT 262 262 L -> V (IN dbSNP:5392).
 FT VARIANT 354 354 /FTid=VAR_011809.
 FT CONFLICT 12 12 E -> Q (IN dbSNP:1800437).
 FT CONFLICT 104 104 /FTid=VAR_011810.
 FT CONFLICT 117 117 R -> G (IN REF. 2).
 FT CONFLICT 137 137 G -> R (IN REF. 2).
 FT CONFLICT 337 337 MISSING (IN REF. 3).
 FT CONFLICT 367 371 L -> V (IN REF. 2).
 FT CONFLICT 367 371 GAURF -> APCV (IN REF. 3).
 FT SEQUENCE 466 AA; 53156 MW; C45CF86BA0E32383 CRC64;
 Query Match 2.2%; Score 12; DB 1; Length 466;
 Best Local Similarity 100.0%; Pred. No. 0.00049;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 169 FRHLHCTRNVIH 180
 Db 162 FRHLHCTRNVIH 173
 RESULT 20
 GLR_HUMAN STANDARD; PRT; 477 AA.
 AC P47871;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glucagon receptor precursor (GL-R).
 GN GCGR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94121651; PubMed=7507321;
 RA Macneil D.J., Occi J.L., Hey P.J., Strader C.D., Graziano M.P.;
 RT "Cloning and expression of a human glucagon receptor.";
 RL Biochem. Biophys. Res. Commun. 198:328-334(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9412999; PubMed=8144028;
 RA Lok S., Kuljper J.L., Jelinek L.J., Kramer J.M., Whitmore T.E.,
 RA Sprecher C.A., Mathews S., Grant F.J., Biggs S.H., Rosenberg G.B.;
 RT "The human glucagon receptor encoding gene: structure, cDNA sequence
 and chromosomal localization.";
 RL Gene 140:203-209(1994).

RN [3]
 RP SEQUENCE OF 21-54 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=9429224; PubMed=8020989;
 RA Menzel S., Stoffel M., Espinosa R. III, Fernald A.A., Le Beau M.M.,
 RA Bell G.I.;
 RT "Localization of the glucagon receptor gene to human chromosome band
 17q25.";
 RL Genomics 20:327-328(1994).
 RN [4]
 RP VARIANT SER-40.
 RX MEDLINE=96034210; PubMed=7589886;
 RA Fujisawa T., Ikegami H., Yamato E., Takekawa K., Nakagawa Y.,
 RA Hamada Y., Ueda H., Fukuda M., Ogihara T.;
 RT "A mutation in the glucagon receptor gene (Gly40Ser): heterogeneity
 in the association with diabetes mellitus.";
 RL Diabetologia 38:983-985(1995).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON WHICH PLAYS A CENTRAL
 CC ROLE IN REGULATING THE LEVEL OF BLOOD GLUCOSE BY CONTROLLING THE
 CC RATE OF HEPATIC GLUCOSE PRODUCTION AND INSULIN SECRETION. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 CC ADENYLATE CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC DISEASE: IT IS A CANDIDATE FOR CERTAIN DEFECTS IN NON-INSULIN-
 CC DEPENDENT DIABETES MELLITUS (NIDDM). THE VARIANT IN POSITION 40
 CC (SER) IS FOUND IN SOME NIDDM PATIENTS, BUT ALSO IN NONDIABETIC
 CC SUBJECTS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; U03469; AAC52063.1; -;
 CC EMBL; L20316; AAA53628.1; -;
 CC EMBL; L24751; AAA35897.1; -;
 CC PIR; JC2041; JC2041
 CC Genew; HGNC:4192; GCGR.
 CC MIM; 138033; -;
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0004967; F:glucagon receptor activity; TAS.
 CC GO; GO:0006091; P:energy pathways; TAS.
 CC GO; GO:0007188; P:G-protein signaling, coupled to cAMP nucleo. . .; TAS.
 CC GO; GO:0007584; P:nutritional response pathway; TAS.
 CC GO; GO:0008217; P:regulation of blood pressure; TAS.
 CC InterPro; IPR000832; GPCR secretin.
 CC InterPro; IPR01879; hormn_receptor.
 CC Pfam; PF00002; 7tm_2; 1.
 CC Pfam; PF02793; HRM; 1.
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; Hormr; 1.
 CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 CC PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
 CC PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Polymorphism; Diabetes mellitus.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 477 GLUCAGON RECEPTOR.
 FT DOMAIN 26 142 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 143 166 1 (POTENTIAL).
 FT DOMAIN 167 173 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 174 193 2 (POTENTIAL).
 FT DOMAIN 194 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 249 3 (POTENTIAL).
 FT DOMAIN 250 283 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 264 285 4 (POTENTIAL).


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FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 326 5 (POTENTIAL).
FT DOMAIN 327 350 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 351 369 6 (POTENTIAL).
FT DOMAIN 370 381 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 382 404 7 (POTENTIAL).
FT DOMAIN 405 477 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 78 78 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 40 40 G -> S (IN dbSNP:1801483).
FT VARIANT 114 114 /FTId=VAR 003581.
FT SEQUENCE 477 AA; 54009 MW; ADBB477C6267AB6E CRC64;

Query Match 1.8%; Score 10; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.056; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 255 LVEGLYLHNL 264
DB 243 LVEGLYLHNL 252

RESULT 21
GLP2_RAT
ID GLP2_RAT STANDARD; PRT; 550 AA.
AC Q9Z0W0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Glucagon-like peptide 2 receptor precursor (GLP-2 receptor) (GLP-2-R) (GLP-2R).
DE (GLP-2R).
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP STRAIN=Sprague-Dawley; TISSUE=Hypothalamus;
RX MEDLINE=99145591; PubMed=990065;
RA Munroe D.G., Gupta A.K., Kooshesh F., Vyas T.B., Rizkalla G., Wang H.,
RA Demchayshyn L., Yang Z.-H., Kamboj R.K., Chen H., McCallum K.,
RA Summer-Smith M., Drucker D.J., Crivici A.;
RT "Prototypic G protein-coupled receptor for the intestinotrophic factor
RT glucagon-like peptide 2";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1569-1574(1999).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 2. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AF105368; AAD16896.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RCEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RCEP_F2_2; FALSE_NEG.
DR PROSITE; PS00227; G_PROTEIN_RCEP_F2_3; 1.

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DR PROSITE; PS50261; G_PROTEIN_RCEP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 1 POTENTIAL.
FT CHAIN ? 550 GLUCAGON-LIKE PEPTIDE 2 RECEPTOR.
FT DOMAIN ? 179 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 180 202 1 (POTENTIAL).
FT DOMAIN 203 210 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 211 230 2 (POTENTIAL).
FT DOMAIN 231 261 3 (POTENTIAL).
FT TRANSMEM 262 286 3 (POTENTIAL).
FT DOMAIN 287 298 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 299 322 4 (POTENTIAL).
FT DOMAIN 323 337 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 338 363 5 (POTENTIAL).
FT DOMAIN 364 385 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 386 406 6 (POTENTIAL).
FT DOMAIN 407 421 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 422 442 7 (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 162 162 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 550 AA; 63102 MW; 22E269F811E25226 CRC64;

Query Match 1.8%; Score 10; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.063; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 172 LHCTRNYYHM 181
DB 206 LHCTRNYYHM 215

RESULT 22
GLP2_HUMAN
ID GLP2_HUMAN STANDARD; PRT; 553 AA.
AC O95838;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Glucagon-like peptide 2 receptor precursor (GLP-2 receptor) (GLP-2-R) (GLP-2R).
DE (GLP-2R).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=99145591; PubMed=990065;
RA Munroe D.G., Gupta A.K., Kooshesh F., Vyas T.B., Rizkalla G., Wang H.,
RA Demchayshyn L., Yang Z.-H., Kamboj R.K., Chen H., McCallum K.,
RA Summer-Smith M., Drucker D.J., Crivici A.;
RT "Prototypic G protein-coupled receptor for the intestinotrophic factor
RT glucagon-like peptide 2";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1569-1574(1999).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 2. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AF105367; AAD16895.1; -.

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RESULT 24

VIPS_RAT STANDARD; PRT; 437 AA.

AC 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Vasoactive intestinal polypeptide receptor 2 precursor (VIP-R-2)

DE (Pituitary adenylate cyclase activating polypeptide type III receptor)

DE (PACAP type III receptor) (PACAP-R-3).

GN VIPR2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Olfactory bulb;

RX MEDLINE=94039806; PubMed=8224221;

RA Lutz E.-M., Sheward W.J., West K.M., Morrow J.A., Fink G., Harmar A.J.;

RA "The VIP2 receptor: molecular characterisation of a cDNA encoding a novel receptor for vasoactive intestinal peptide.";

RL FEBS Lett. 334:3-8(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain cortex;

RX MEDLINE=95080140; PubMed=7988457;

RA Usdin T.B., Bonner T.I., Mezey E.;

RA "Two receptors for vasoactive intestinal polypeptide with similar specificity and complementary distributions.";

RL Endocrinology 135:2662-2680(1994).

CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27, THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE. CAN BE COUPLED TO PHOSPHOLIPASE C.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL; Z25885; CAA81104.1; -;

DR EMBL; U09631; AAB60459.1; -;

DR F01; S39069; S39069.

DR InterPro; IPR000832; GPCR secretin.

DR Pfam; PF00002; 7tm_2; 1.

DR Pfam; PF02793; HRM; 1.

DR PRINTS; PR00249; GPCRSECRETIN.

DR SMART; SM00008; Hormr; 1.

DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.

DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 22

FT CHAIN 23 437

FT VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2.

FT DOMAIN 23 125

FT TRANSMEM 126 150

FT DOMAIN 151 157

FT CYTOPLASMIC (POTENTIAL). 2 (POTENTIAL).

FT TRANSMEM 158 177

FT DOMAIN 178 202

FT TRANSMEM 203 226

FT DOMAIN 227 239

FT CYTOPLASMIC (POTENTIAL). 4 (POTENTIAL).

FT TRANSMEM 240 261

FT DOMAIN 262 278

FT TRANSMEM 279 302

FT DOMAIN 303 327

FT TRANSMEM 328 347

FT DOMAIN 348 359

FT TRANSMEM 360 379

FT DOMAIN 380 437

FT DISULFID 201 270

FT CARBOHYD 57 57

FT CARBOHYD 87 87

FT CARBOHYD 91 91

FT CONFLICT 383 383

SQ SEQUENCE 437 AA; 49552 MM; 7E10218A9BE31360 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 437;

Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0;

QY 172 LHCTRNYYH 180

DB 153 LHCTRNYYH 161

RESULT 25

VIPS_HUMAN STANDARD; PRT; 438 AA.

ID VIPS_HUMAN STANDARD; PRT; 438 AA.

AC P41587; Q13053; Q15870;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Vasoactive intestinal polypeptide receptor 2 precursor (VIP-R-2)

DE (Pituitary adenylate cyclase activating polypeptide type III receptor)

DE (PACAP type III receptor) (PACAP-R-3) (Helodermin-preferring VIP receptor).

DE VIPR2 OR VIP2R.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95110300; PubMed=7811244;

RA Svoboda M., Tastenoy M., van Rampelbergh J., Goossens J.-F., Neef P., Waelbroeck M., Robberecht P.;

RA "Molecular cloning and functional characterization of a human VIP receptor from SUP-T1 lymphoblasts.";

RL Biochem. Biophys. Res. Commun. 205:1617-1624(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97092885; PubMed=8938447;

RA Mackay M., Fantes J., Scherer S., Boyle S., West K., Tsui L.C., Belloni E., Lutz E., van Heyningen V., Harmar A.J.;

RA "Chromosomal localization in mouse and human of the vasoactive intestinal peptide receptor type 2 gene: a possible contributor to the holoprosencephaly 3 phenotype.";

RL Genomics 37:345-353(1996).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=97087354; PubMed=8933357;

RA Wei Y., Mojsos S.;

RA "Tissue specific expression of different human receptor types for pituitary adenylate cyclase activating polypeptide and vasoactive intestinal polypeptide: implications for their role in human physiology.";

RL J. Neuroendocrinol. 8:811-817(1996).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=99412192; PubMed=10481065;

RA Lutz E.M., Shen S., Mackay M., West K., Harmar A.J.;

RA "Structure of the human VIP2R gene for vasoactive intestinal peptide type 2 receptor.";

RL FEBS Lett. 458:197-203(1999).

RN RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.F., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Valladao D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27,
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
 CC ACTIVATE ADENYLYL CYCLASE. CAN BE COUPLED TO PHOSPHOLIPASE C.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; LA0764; AAC41756.1; -
 DR EMBL; L36566; AAC37569.1; -
 DR EMBL; X95097; CAA64474.1; -
 DR EMBL; U13810; AAC50872.1; -
 DR EMBL; Y18423; CAB41899.1; -
 DR EMBL; Y18424; CAB41899.1; JOINED.
 DR EMBL; Y18425; CAB41899.1; JOINED.
 DR EMBL; Y18426; CAB41899.1; JOINED.
 DR EMBL; Y18427; CAB41899.1; JOINED.
 DR EMBL; Y18428; CAB41899.1; JOINED.
 DR EMBL; Y18429; CAB41899.1; JOINED.
 DR EMBL; Y18430; CAB41899.1; JOINED.
 DR EMBL; Y18431; CAB41899.1; JOINED.
 DR EMBL; BC010569; AAH10569.1; -
 DR PIR; G02822; G02822.
 DR Genew; HGNC:12695; VIPR2.
 DR MIM; 601970; -
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; horum_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECIP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECIP_F2_2; 1.
 DR PROSITE; PS00651; G_PROTEIN_RECIP_F2_3; 1.
 DR PROSITE; PS00652; G_PROTEIN_RECIP_F2_4; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Polymorphism. 1 23 POTENTIAL.
 SIGNAL 24 438 VASOACTIVE INTESTINAL POLYPEPTIDE
 FT CHAIN

FT DOMAIN 24 126
 FT TRANSSEM 127 151
 FT DOMAIN 152 158
 FT TRANSSEM 159 178
 FT DOMAIN 179 203
 FT TRANSSEM 204 227
 FT DOMAIN 228 241
 FT TRANSSEM 241 262
 FT DOMAIN 263 279
 FT TRANSSEM 280 303
 FT TRANSSEM 304 328
 FT TRANSSEM 329 348
 FT DOMAIN 349 360
 FT TRANSSEM 361 380
 FT DOMAIN 381 438
 FT DISULFID 202 271
 FT CARBOHYD 58 58
 FT CARBOHYD 88 88
 FT CARBOHYD 92 92
 FT VARIANT 39 39
 FT VARIANT 412 412
 FT CONFLICT 424 424
 FT SEQUENCE 438 AA; 49478 MW; 265A43A70BE09699 CRC64;
 SQ SEQUENCE 438 AA; 49478 MW; 265A43A70BE09699 CRC64;
 Query Match 1-7%; Score 9; DB 1; Length 438;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 172 LHCTRYNIIH 180
 DB 154 LHCTRYNIIH 162
 RESULT 26
 ID GLPI_HUMAN STANDARD; PRT; 463 AA.
 AC P43220; Q99669;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glucagon-like peptide 1 receptor precursor (GLP-1 receptor) (GLP-1-R)
 DE (GLP-1R).
 GN GLP1R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancratic islets;
 RX MEDLINE=9400966; PubMed=8405712;
 RA Thorens B., Porret A., Buehler L., Deng S., Morel P., Widmann C.;
 RT "Cloning and functional expression of the human islet GLP-1 receptor.
 RT Demonstration that extendin-4 is an agonist and extendin-(9-39) an
 RT antagonist of the receptor.";
 RL Diabetes 42:1678-1682 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancratic islets;
 RX MEDLINE=94008746; PubMed=8404634;
 RA Dillon J.S., Tanizawa Y., Wheeler M.B., Leng X., Ligon B.B.,
 RA Rabin D.U., Yoo-Warren H., Permutt M., Boyd A.E.;
 RT "Cloning and functional expression of the human glucagon-like
 RT peptide-1 (GLP-1) receptor.";
 RL Endocrinology 133:1907-1910 (1993).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT LEU-260.
 RC TISSUE=Gastric carcinoma;
 RX MEDLINE=94029985; PubMed=8216285;
 RA Graziano M.P., Hey P.J., Borkowski D., Chicchi G.C., Strader C.D.;

RT "Cloning and functional expression of a human glucagon-like peptide-1
receptor.";
RL Biochem. Biophys. Res. Commun. 196;141-146(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Insulinoma; PubMed=7517895;
RX MEDLINE=94298957; PubMed=7517895;
RA van Eyll B., Lankat-Buttgereit B., Bode H.P., Goetze R., Goetze B.;
RT "Signal transduction of the GLP-1-receptor cloned from a human
insulinoma.";
RL FEBS Lett. 348:7-13(1994).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT LEU-260.
RC TISSUE=Pancreas;
RX MEDLINE=95145713; PubMed=7843404;
RA Wei Y., Mojsos S.;
RT "Tissue-specific expression of the human receptor for glucagon-like
peptide-1: brain, heart and pancreatic forms have the same deduced
amino acid sequences.";
RL FEBS Lett. 358:219-224(1995).
RN [6]
RP SEQUENCE FROM N.A., AND VARIANT LEU-260.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A., AND VARIANT LEU-260.
RA Smalley C.;
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 1-26 FROM N.A.
RC TISSUE=Placenta;
RA Lankat-Buttgereit B., Goetze B.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 1. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYLYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; U01104; AAA03614.1; -;
CC EMBL; U01157; AAA62471.1; -;
CC EMBL; U01156; AAC50050.1; -;
CC EMBL; L23503; AAA17021.1; -;
CC EMBL; U10037; AAA63787.1; -;
CC EMBL; AB065685; BAC05908.1; -;
CC EMBL; AL035690; CAB71177.1; -;
CC EMBL; U66062; AAB64013.1; -;
CC PIR; I84494; I84494.
CC PIR; S71624; S71624.
CC Genew; HGNC:4324; GLP1R.
CC MIM; 138032; -;
CC GO; GO:0016021; C:integral to membrane; TAS.
CC DR GO; GO:0005886; C:plasma membrane; TAS.
CC DR GO; GO:0007190; P:adenylate cyclase activation; TAS.
CC DR InterPro; IPR000832; GPCR_secretin.
CC DR InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm 2; 1.
CC Pfam; PF02793; HRM; 1.
CC DR PRINTS; PR00249; GPCRSECRETIN.
CC DR SMART; SM00008; Hormr; 1.
CC DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

DR PROSITE; PS02027; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS02061; G_PROTEIN_RECEP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Polymorphism.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 463 GLUCAGON-LIKE PEPTIDE 1 RECEPTOR.
FT DOMAIN 24 145 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 146 168 1 (POTENTIAL).
FT DOMAIN 169 176 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 177 196 2 (POTENTIAL).
FT DOMAIN 197 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 252 3 (POTENTIAL).
FT DOMAIN 253 264 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 265 288 4 (POTENTIAL).
FT DOMAIN 289 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 329 5 (POTENTIAL).
FT DOMAIN 330 351 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 352 372 6 (POTENTIAL).
FT DOMAIN 373 387 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 388 408 7 (POTENTIAL).
FT DOMAIN 409 463 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 260 260 P -> L.
FT /FTID=VAR_015098.
FT CONFLICT 12 12 L -> V (IN REF. 1, 4 AND 7).
FT CONFLICT 136 137 SP -> WG (IN REF. 1).
FT CONFLICT 137 137 P -> R (IN REF. 4).
FT CONFLICT 151 151 G -> A (IN REF. 1).
FT CONFLICT 221 221 Q -> L (IN REF. 5).
FT CONFLICT 289 289 Y -> I (IN REF. 1).
FT CONFLICT 316 316 A -> G (IN REF. 2).
SQ SEQUENCE 463 AA; 53059 MW; 04DB63C68E54DD55 CRC64;
Query Match 1.7%; Score 9; DB 1; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 172 LHCTRNVIH 180
Db 172 LHCTRNVIH 180
RESULT 27
GLP1_RAT
ID GLP1_RAT STANDARD; PRT; 463 AA.
AC P32301; Q64073.1
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucagon-like peptide 1 receptor precursor (GLP-1 receptor) (GLP-1-R)
DE (GLP-1R).
GN GLP1R OR GLPR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95112989; PubMed=7813606;
RA Lankat-Buttgereit B., Goke R., Fehmann H.C., Richter G., Goke B.;
RT "Expression cloning of the pancreatic beta cell receptor for the
gluco-incretin hormone glucagon-like peptide 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:8641-8645(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95112989; PubMed=7813606;
RA Lankat-Buttgereit B., Goke R., Fehmann H.C., Richter G., Goke B.;
RT "Molecular cloning of a cDNA encoding for the GLP-1 receptor
expressed in rat lung.";

```

RL Exp. Clin. Endocrinol. 102:341-347(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 1. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYLIL CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: PANCREATIC ISLETS, STOMACH, LUNG, RAT
CC INSULINOMA CELL LINE.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; M97797; AAA73377.1; -.
CC EMBL; S75952; -. NOT ANNOTATED_CDS.
CC PIR; A46172; A46172; GPCR_secretin.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00645; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 21 POTENTIAL.
CC CHAIN 22 463 GLUCAGON-LIKE PEPTIDE 1 RECEPTOR.
CC DOMAIN 22 145 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 146 168 1 (POTENTIAL).
CC DOMAIN 169 176 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 177 196 2 (POTENTIAL).
CC DOMAIN 197 227 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 228 252 3 (POTENTIAL).
CC DOMAIN 253 264 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 265 288 4 (POTENTIAL).
CC DOMAIN 289 303 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 304 329 5 (POTENTIAL).
CC DOMAIN 330 351 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 352 372 6 (POTENTIAL).
CC DOMAIN 373 387 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 388 408 7 (POTENTIAL).
CC DOMAIN 409 463 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CONFLICT 323 323 V -> I (IN REF. 2).
CC SEQUENCE 463 AA; 52876 MW; ABE21838EBE621F CRC64;

Query Match 1.7%; Score 9; DB 1; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.58; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 172 LHCTRYNIIH 180
| | | | |
Db 172 LHCTRYNIIH 180

RESULT 28
PACR HUMAN
ID _PACR_HUMAN STANDARD; PRT; 468 AA.
AC P41586;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide type I receptor
DE precursor (PACAP type I receptor) (PACAP-R-1).
GN ADCYAP1R1.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=94071916; PubMed=7902709;
RA Ogi K., Miyamoto Y., Masuda Y., Habata Y., Hosoya M., Ohtaki T.,
RA Masuo Y., Onda H., Fujino M.;
RT "Molecular cloning and functional expression of a cDNA encoding a
RT human pituitary adenylate cyclase activating polypeptide receptor.";
RL Biochem. Biophys. Res. Commun. 196:1511-1521(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tezumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 418-468 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95154842; PubMed=7851900;
RA Scofield M., Espinosa R., Trabb J.B., le Beau M.M., Bell G.I.;
RT "Human type I pituitary adenylate cyclase activating polypeptide
RT receptor (ADCYAP1R): localization to chromosome band 7p14 and
RT integration into the cytogenetic, physical and genetic map of
RT chromosome 7.";
RL Genomics 23:697-699(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLIL CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,
CC LUTEINIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND
CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM
CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE
CC GASTROINTESTINAL TRACT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN THE BRAIN, LOW EXPRESSION IN
CC THE LUNG, LIVER, THYMUS, SPLEEN, PANCREAS AND PLACENTA.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D17516; BAA04466.1; ALT INIT.
CC EMBL; AB065700; BAC05923.1; -.
CC EMBL; U09216; AAA19323.1; -.
CC Genew; HGNC:242; ADCYAP1R1.
CC MIM; 102981; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004872; F:receptor activity; TAS.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Spermatoogenesis.
CC SIGNAL 1 20 POTENTIAL.
CC CHAIN 21 468 PITUITARY ADENYLATE CYCLASE ACTIVATING
CC DOMAIN 21 155 POLYPEPTIDE TYPE I RECEPTOR.
CC EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 156 178 1 (POTENTIAL).
FT DOMAIN 179 186 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 187 205 2 (POTENTIAL).
FT DOMAIN 206 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 253 3 (POTENTIAL).
FT DOMAIN 254 268 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 269 291 4 (POTENTIAL).
FT DOMAIN 292 309 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 310 332 5 (POTENTIAL).
FT DOMAIN 333 350 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 351 371 6 (POTENTIAL).
FT DOMAIN 372 385 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 386 405 7 (POTENTIAL).
FT DOMAIN 406 468 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 468 AA; 53313 MW; B5515B84E9F28977 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 LFVSMFLRA 191
    |||||
Db 192 LFVSMFLRA 200

RESULT 29
GLR_MOUSE
ID GLR_MOUSE STANDARD; PRT; 485 AA.
AC Q61606; O63960;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucagon receptor precursor (GL-R).
GN GCGR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96069600; PubMed=7590348;
RA Burcelin R., Li J., Charron M.J.;
RT "Cloning and sequence analysis of the murine glucagon receptor-
encoding gene.";
RL Gene 164:305-310(1995).
RN [2]
RP SEQUENCE OF 324-458 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94208442; PubMed=8156917;
RA Campos R.V., Lee Y.C., Drucker D.J.;
RT "Divergent tissue-specific and developmental expression of receptors
for glucagon and glucagon-like peptide-1 in the mouse.";
RL Endocrinology 134:2156-2164(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON WHICH PLAYS A CENTRAL
CC ROLE IN REGULATING THE LEVEL OF BLOOD GLUCOSE BY CONTROLLING THE
CC RATE OF HEPATIC GLUCOSE PRODUCTION AND INSULIN SECRETION. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LIVER, KIDNEY,
CC ADRENAL, LUNG AND STOMACH, WHILE LOWER LEVELS OF EXPRESSION ARE
CC DETECTED IN BROWN AND WHITE ADIPOSE TISSUE, CEREBELLUM, DUODENUM
CC AND HEART.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
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DR EMBL; S69384; AAB30529.2; -.
DR PIR; JC4363; JC4363.
DR MGD; MGI:99572; GCGR.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
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DR Pfam; PF02793; HRM; 1.
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DR PROSITE; PS00919; G_PROTEIN_RECP_F2_271; 1.
DR PROSITE; PS00920; G_PROTEIN_RECP_F2_272; 1.
DR PROSITE; PS00921; G_PROTEIN_RECP_F2_273; 1.
DR PROSITE; PS00922; G_PROTEIN_RECP_F2_274; 1.
DR PROSITE; PS00923; G_PROTEIN_RECP_F2_275; 1.
DR PROSITE; PS00924; G_PROTEIN_RECP_F2_276; 1.
DR PROSITE; PS00925; G_PROTEIN_RECP_F2_277; 1.
DR PROSITE; PS00926; G_PROTEIN_RECP_F2_278; 1.
DR PROSITE; PS00927; G_PROTEIN_RECP_F2_279; 1.
DR PROSITE; PS00928; G_PROTEIN_RECP_F2_280; 1.
DR PROSITE; PS00929; G_PROTEIN_RECP_F2_281; 1.
DR PROSITE; PS00930; G_PROTEIN_RECP_F2_282; 1.
DR PROSITE; PS00931; G_PROTEIN_RECP_F2_283; 1.
DR PROSITE; PS00932; G_PROTEIN_RECP_F2_284; 1.
DR PROSITE; PS00933; G_PROTEIN_RECP_F2_285; 1.
DR PROSITE; PS00934; G_PROTEIN_RECP_F2_286; 1.
DR PROSITE; PS00935; G_PROTEIN_RECP_F2_287; 1.
DR PROSITE; PS00936; G_PROTEIN_RECP_F2_288; 1.
DR PROSITE; PS00937; G_PROTEIN_RECP_F2_289; 1.
DR PROSITE; PS00938; G_PROTEIN_RECP_F2_290; 1.
DR PROSITE; PS00939; G_PROTEIN_RECP_F2_291; 1.
DR PROSITE; PS00940; G_PROTEIN_RECP_F2_292; 1.
DR PROSITE; PS00941; G_PROTEIN_RECP_F2_293; 1.
DR PROSITE; PS00942; G_PROTEIN_RECP_F2_294; 1.
DR PROSITE; PS00943; G_PROTEIN_RECP_F2_295; 1.
DR PROSITE; PS00944; G_PROTEIN_RECP_F2_296; 1.
DR PROSITE; PS00945; G_PROTEIN_RECP_F2_297; 1.
DR PROSITE; PS00946; G_PROTEIN_RECP_F2_298; 1.
DR PROSITE; PS00947; G_PROTEIN_RECP_F2_299; 1.
DR PROSITE; PS00948; G_PROTEIN_RECP_F2_300; 1.
DR PROSITE; PS00949; G_PROTEIN_RECP_F2_301; 1.
DR PROSITE; PS00950; G_PROTEIN_RECP_F2_302; 1.
DR PROSITE; PS00951; G_PROTEIN_RECP_F2_303; 1.
DR PROSITE; PS00952; G_PROTEIN_RECP_F2_304; 1.
DR PROSITE; PS00953; G_PROTEIN_RECP_F2_305; 1.
DR PROSITE; PS00954; G_PROTEIN_RECP_F2_306; 1.
DR PROSITE; PS00955; G_PROTEIN_RECP_F2_307; 1.
DR PROSITE; PS00956; G_PROTEIN_RECP_F2_308; 1.
DR PROSITE; PS00957; G_PROTEIN_RECP_F2_309; 1.
DR PROSITE; PS00958; G_PROTEIN_RECP_F2_310; 1.
DR PROSITE; PS00959; G_PROTEIN_RECP_F2_311; 1.
DR PROSITE; PS00960; G_PROTEIN_RECP_F2_312; 1.
DR PROSITE; PS00961; G_PROTEIN_RECP_F2_313; 1.
DR PROSITE; PS00962; G_PROTEIN_RECP_F2_314; 1.
DR PROSITE; PS00963; G_PROTEIN_RECP_F2_315; 1.
DR PROSITE; PS00964; G_PROTEIN_RECP_F2_316; 1.
DR PROSITE; PS00965; G_PROTEIN_RECP_F2_317; 1.
DR PROSITE; PS00966; G_PROTEIN_RECP_F2_318; 1.
DR PROSITE; PS00967; G_PROTEIN_RECP_F2_319; 1.
DR PROSITE; PS00968; G_PROTEIN_RECP_F2_320; 1.
DR PROSITE; PS00969; G_PROTEIN_RECP_F2_321; 1.
DR PROSITE; PS00970; G_PROTEIN_RECP_F2_322; 1.
DR PROSITE; PS00971; G_PROTEIN_RECP_F2_323; 1.
DR PROSITE; PS00972; G_PROTEIN_RECP_F2_324; 1.
DR PROSITE; PS00973; G_PROTEIN_RECP_F2_325; 1.
DR PROSITE; PS00974; G_PROTEIN_RECP_F2_326; 1.
DR PROSITE; PS00975; G_PROTEIN_RECP_F2_327; 1.
DR PROSITE; PS00976; G_PROTEIN_RECP_F2_328; 1.
DR PROSITE; PS00977; G_PROTEIN_RECP_F2_329; 1.
DR PROSITE; PS00978; G_PROTEIN_RECP_F2_330; 1.
DR PROSITE; PS00979; G_PROTEIN_RECP_F2_331; 1.
DR PROSITE; PS00980; G_PROTEIN_RECP_F2_332; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F2_333; 1.
DR PROSITE; PS00982; G_PROTEIN_RECP_F2_334; 1.
DR PROSITE; PS00983; G_PROTEIN_RECP_F2_335; 1.
DR PROSITE; PS00984; G_PROTEIN_RECP_F2_336; 1.
DR PROSITE; PS00985; G_PROTEIN_RECP_F2_337; 1.
DR PROSITE; PS00986; G_PROTEIN_RECP_F2_338; 1.
DR PROSITE; PS00987; G_PROTEIN_RECP_F2_339; 1.
DR PROSITE; PS00988; G_PROTEIN_RECP_F2_340; 1.
DR PROSITE; PS00989; G_PROTEIN_RECP_F2_341; 1.
DR PROSITE; PS00990; G_PROTEIN_RECP_F2_342; 1.
DR PROSITE; PS00991; G_PROTEIN_RECP_F2_343; 1.
DR PROSITE; PS00992; G_PROTEIN_RECP_F2_344; 1.
DR PROSITE; PS00993; G_PROTEIN_RECP_F2_345; 1.
DR PROSITE; PS00994; G_PROTEIN_RECP_F2_346; 1.
DR PROSITE; PS00995; G_PROTEIN_RECP_F2_347; 1.
DR PROSITE; PS00996; G_PROTEIN_RECP_F2_348; 1.
DR PROSITE; PS00997; G_PROTEIN_RECP_F2_349; 1.
DR PROSITE; PS00998; G_PROTEIN_RECP_F2_350; 1.
DR PROSITE; PS00999; G_PROTEIN_RECP_F2_351; 1.
DR PROSITE; PS01000; G_PROTEIN_RECP_F2_352; 1.
DR PROSITE; PS01001; G_PROTEIN_RECP_F2_353; 1.
DR PROSITE; PS01002; G_PROTEIN_RECP_F2_354; 1.
DR PROSITE; PS01003; G_PROTEIN_RECP_F2_355; 1.
DR PROSITE; PS01004; G_PROTEIN_RECP_F2_356; 1.
DR PROSITE; PS01005; G_PROTEIN_RECP_F2_357; 1.
DR PROSITE; PS01006; G_PROTEIN_RECP_F2_358; 1.
DR PROSITE; PS01007; G_PROTEIN_RECP_F2_359; 1.
DR PROSITE; PS01008; G_PROTEIN_RECP_F2_360; 1.
DR PROSITE; PS01009; G_PROTEIN_RECP_F2_361; 1.
DR PROSITE; PS01010; G_PROTEIN_RECP_F2_362; 1.
DR PROSITE; PS01011; G_PROTEIN_RECP_F2_363; 1.
DR PROSITE; PS01012; G_PROTEIN_RECP_F2_364; 1.
DR PROSITE; PS01013; G_PROTEIN_RECP_F2_365; 1.
DR PROSITE; PS01014; G_PROTEIN_RECP_F2_366; 1.
DR PROSITE; PS01015; G_PROTEIN_RECP_F2_367; 1.
DR PROSITE; PS01016; G_PROTEIN_RECP_F2_368; 1.
DR PROSITE; PS01017; G_PROTEIN_RECP_F2_369; 1.
DR PROSITE; PS01018; G_PROTEIN_RECP_F2_370; 1.
DR PROSITE; PS01019; G_PROTEIN_RECP_F2_371; 1.
DR PROSITE; PS01020; G_PROTEIN_RECP_F2_372; 1.
DR PROSITE; PS01021; G_PROTEIN_RECP_F2_373; 1.
DR PROSITE; PS01022; G_PROTEIN_RECP_F2_374; 1.
DR PROSITE; PS01023; G_PROTEIN_RECP_F2_375; 1.
DR PROSITE; PS01024; G_PROTEIN_RECP_F2_376; 1.
DR PROSITE; PS01025; G_PROTEIN_RECP_F2_377; 1.
DR PROSITE; PS01026; G_PROTEIN_RECP_F2_378; 1.
DR PROSITE; PS01027; G_PROTEIN_RECP_F2_379; 1.
DR PROSITE; PS01028; G_PROTEIN_RECP_F2_380; 1.
DR PROSITE; PS01029; G_PROTEIN_RECP_F2_381; 1.
DR PROSITE; PS01030; G_PROTEIN_RECP_F2_382; 1.
DR PROSITE; PS01031; G_PROTEIN_RECP_F2_383; 1.
DR PROSITE; PS01032; G_PROTEIN_RECP_F2_384; 1.
DR PROSITE; PS01033; G_PROTEIN_RECP_F
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RA Jelinek L.J., Lok S., Grant F.J., Rosenberg G.B., Smith R.A.,
 RA Benach P.A., Sheppard P.O., O'Hara P.J., Foster D.C.,
 RA Kuiper J.L., Biggs S.H., Walker K.M., Chen L.H., McKernan P.A.,
 RA Kindsvogel W.,
 RT "Expression cloning and signaling properties of the rat glucagon
 RT receptor.",
 RL Science 259:1614-1616(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93213282; PubMed=8384842;
 RA Svoboda M., Ciccarelli E., Tastenoy M., Cauvin A., Stievenart M.,
 RA Christophe J.,
 RT "Small introns in a hepatic cDNA encoding a new glucagon-like peptide
 RT 1-type receptor.",
 RL Biochem. Biophys. Res. Commun. 191:479-486(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=liver;
 RX MEDLINE=94364484; PubMed=8082779;
 RA Maget B., Tastenoy M., Svoboda M.,
 RT "Sequencing of eleven introns in genomic DNA encoding rat glucagon
 RT receptor and multiple alternative splicing of its mRNA.",
 RL FEBS Lett. 351:271-275(1994).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON WHICH PLAYS A CENTRAL
 CC ROLE IN REGULATING THE LEVEL OF BLOOD GLUCOSE BY CONTROLLING THE
 CC RATE OF HEPATIC GLUCOSE PRODUCTION AND INSULIN SECRETION. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 CC ADENYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL; L04796; AAA16439.1; -
 DR EMBL; X68692; AAA48651.1; -
 DR EMBL; M96674; AAA02392.1; -
 DR EMBL; U63021; AAB16800.1; -
 DR PIR; JQ1957; JQ1957.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM_1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hornr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 485
 FT DOMAIN 27 143
 FT TRANSMEM 144 167
 FT TRANSMEM 168 174
 FT TRANSMEM 175 194
 FT TRANSMEM 195 226
 FT TRANSMEM 227 250
 FT TRANSMEM 251 264
 FT TRANSMEM 265 286
 FT TRANSMEM 287 304
 FT TRANSMEM 305 327
 FT TRANSMEM 328 352
 FT TRANSMEM 352 370
 FT TRANSMEM 371 382
 FT TRANSMEM 383 405
 FT TRANSMEM 406 485

FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 216 216 W -> C (IN REF. 2).
 FT CONFLICT 324 324 V -> A (IN REF. 2).
 SQ SEQUENCE 485 AA; 55038 MW; 91AC67D7A4F5090E CRC64;
 Query Match 1.7%; Score 9; DB 1; Length 485;
 Best Local Similarity 100.0%; Pred.No. 0.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 172 LHCTRNVIH 180
 |||||
 Db 170 LHCTRNVIH 178
 RESULT 31
 GLP1_MOUSE
 ID_GLPI_MOUSE STANDARD; PRT; 489 AA.
 AC O35659;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glucagon-like peptide 1 receptor precursor (GLP-1 receptor) (GLP-1-R)
 DE (GLP-1R).
 GN GLPIR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBT_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=98227650; PubMed=9568699;
 RA Flamez D., van Breusegem A., Scrocchi L.A., Quartier E., Pipeleers D.,
 RA Drucker D.J., Schuit F.,
 RT "Mouse pancreatic beta-cells exhibit preserved glucose competence
 RT after disruption of the glucagon-like peptide-1 receptor gene.",
 RL Diabetes 47:646-652(1998).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 1. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
 CC ACTIVATE ADENYL CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ001692; CAA04930.1; -
 DR MGD; MGI:99571; Glplr.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM_1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hornr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 489
 FT DOMAIN 22 145
 FT TRANSMEM 146 168
 FT TRANSMEM 169 176
 FT TRANSMEM 177 196

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FT DOMAIN 197 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 252 3 (POTENTIAL).
FT DOMAIN 253 264 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 265 288 4 (POTENTIAL).
FT DOMAIN 289 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 329 5 (POTENTIAL).
FT DOMAIN 330 351 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 352 372 6 (POTENTIAL).
FT DOMAIN 373 387 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 388 408 7 (POTENTIAL).
FT DOMAIN 409 489 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 489 AA; 55878 MW; A859487F2D0ED041 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNIIH 180
DB 172 LHCTRNIIH 180
|||||

RESULT 32
PACR MOUSE
ID PACR MOUSE STANDARD; PRT; 496 AA.
AC P70205;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide type I receptor
DE precursor (PACAP type I receptor) (PACAP-R-1).
GN ADCYAP1R1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96256640; PubMed=8664310;
RA Hashimoto H., Yamamoto K., Hagigara N., Ogawa N., Nishino A.,
RA Aino H., Nogi H., Imanishi K., Matsuda T., Baba A.;
RT "cDNA cloning of a mouse pituitary adenylate cyclase-activating
RT polypeptide receptor."
RL Biochim. Biophys. Acta 1281:129-133 (1996).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,
CC LUTEINIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND
CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM
CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE
CC GASTROINTESTINAL TRACT.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; D82935; BAA11639.1; -
CC MGD; MGI:108449; Adcyap1r1.
CC InterPro; IPR000832; GPCR secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.

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DR PROSITE; PS00649; G PROTEIN RECP F2_1; 1.
DR PROSITE; PS00650; G PROTEIN RECP F2_2; 1.
DR PROSITE; PS00651; G PROTEIN RECP F2_3; 1.
DR PROSITE; PS00652; G PROTEIN RECP F2_4; 1.
DR PROSITE; PS00653; G PROTEIN RECP F2_5; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Spermatogenesis.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 496 PITUITARY ADENYLATE CYCLASE ACTIVATING
FT POLYPEPTIDE TYPE I RECEPTOR.
FT DOMAIN 21 155 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 156 178 1 (POTENTIAL).
FT DOMAIN 179 186 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 187 205 2 (POTENTIAL).
FT DOMAIN 206 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 253 3 (POTENTIAL).
FT DOMAIN 254 268 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 269 291 4 (POTENTIAL).
FT DOMAIN 292 309 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 310 332 5 (POTENTIAL).
FT DOMAIN 333 378 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 379 399 6 (POTENTIAL).
FT DOMAIN 400 413 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 414 433 7 (POTENTIAL).
FT DOMAIN 434 496 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 496 AA; 56639 MW; 47B5D51D4209060A CRC64;

Query Match 1.7%; Score 9; DB 1; Length 496;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSMLEA 191
DB 192 LFVSMLEA 200
|||||

RESULT 33
PACR BOVIN
ID PACR BOVIN STANDARD; PRT; 513 AA.
AC Q29627;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide type I receptor
DE precursor (PACAP type I receptor) (PACAP-R-1).
GN ADCYAP1R1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Brain;
RX MEDLINE=94325336; PubMed=8049255;
RA Miyamoto Y., Habata Y., Ohtaki T., Masuda Y., Ogi K., Onda H.,
RA Fujino M.;
RT "Cloning and expression of a complementary DNA encoding the bovine
RT receptor for pituitary adenylate cyclase-activating polypeptide
RT (PACAP).";
RL Biochim. Biophys. Acta 1218:297-307 (1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,
CC LUTEINIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND
CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM
CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE
CC GASTROINTESTINAL TRACT (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;

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CC CC Comment=Additional isoforms seem to exist;
CC CC Name=Long;
CC CC IsoId=Q29627-1; Sequence=Displayed;
CC CC Name=Short;
CC CC IsoId=Q29627-2; Sequence=VSP_002004;
CC CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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CC CC -----
CC CC EMBL; D17290; BAA04122.1; -;
CC CC EMBL; D17290; BAA04123.1; -;
CC CC PIR; S47631; S47631.
CC CC InterPro; IPR000832; GPCR secretin.
CC CC InterPro; IPR001879; hormn_receptor.
CC CC Pfam; PF00002; 7tm_2; 1.
CC CC Pfam; PF02793; HRM; 1.
CC CC PRINTS; PR00249; GPCRSECRETIN.
CC CC SMART; SM00008; Hormr; 1.
CC CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
CC CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
CC CC PROSITE; PS00650; G_PROTEIN_RECP_F2_3; 1.
CC CC PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
CC CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC CC Alternative splicing.
CC CC SIGNAL 1 37 POTENTIAL.
CC CC CHAIN 38 513 PITUITARY ADENYLATE CYCLASE ACTIVATING
CC CC POLYPEPTIDE TYPE I RECEPTOR.
CC CC DOMAIN 38 172 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 173 195 1 (POTENTIAL).
CC CC DOMAIN 196 203 CYTOPLASMIC (POTENTIAL).
CC CC TRANSMEM 204 222 2 (POTENTIAL).
CC CC DOMAIN 223 244 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 245 270 3 (POTENTIAL).
CC CC DOMAIN 271 285 CYTOPLASMIC (POTENTIAL).
CC CC TRANSMEM 286 308 4 (POTENTIAL).
CC CC DOMAIN 309 326 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 327 349 5 (POTENTIAL).
CC CC DOMAIN 350 395 CYTOPLASMIC (POTENTIAL).
CC CC TRANSMEM 396 416 6 (POTENTIAL).
CC CC DOMAIN 417 430 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 431 450 7 (POTENTIAL).
CC CC DOMAIN 451 513 CYTOPLASMIC (POTENTIAL).
CC CC CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC VARSPLIC 366 393 Missing (in isoform Short).
CC CC SEQUENCE 513 AA; 58785 MW; 9A45753210CE9817 CRC64;
CC CC Query Match 1.7%; Score 9; DB 1; Length 513;
CC CC Best Local Similarity 100.0%; Pred. No. 0.63;
CC CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 183 LFVSEMLRA 191
Db 209 LFVSEMLRA 217
|||||
RESULT 34
PACR_RAT
ID PACR_RAT STANDARD; PRT; 523 AA.
AC P32215; Q63414;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide type IA receptor
DE precursor (PACAP type IA receptor) (PACAP-R-1).

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GN ADCYAP1R1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA MEDLINE=93317678; PubMed=8332197;
RA Wank S.A., Pisegna J.R.;
RT "Molecular cloning and functional expression of the pituitary
RL adenylate cyclase-activating polypeptide type I receptor.";
Proc. Natl. Acad. Sci. U.S.A. 90:6345-6349(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=93326107; PubMed=7687425;
RA Hosoya M., Onda H., Ogi K., Masuda Y., Miyamoto Y., Ohtaki T.,
RA Okazaki H., Arimura A., Fujino M.;
RT "Molecular cloning and functional expression of rat cDNAs encoding
RL the receptor for pituitary adenylate cyclase activating polypeptide
RT (PACAP).";
RL Biochem. Biophys. Res. Commun. 194:133-143(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RA MEDLINE=93357025; PubMed=8394723;
RA Hashimoto H., Ishihara T., Shigemoto R., Mori K., Nagata S.;
RT "Molecular cloning and tissue distribution of a receptor for
RL pituitary adenylate cyclase-activating polypeptide.";
Neuron 11:333-342(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RA MEDLINE=93382505; PubMed=8396727;
RA Spengler D., Waerber C., Pantaloni C., Holsboer F., Bockaert J.,
RA Seeburg P.H., Journot L.;
RT "Differential signal transduction by five splice variants of the
RL PACAP receptor.";
RL Nature 365:170-175(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Olfactory bulb;
RA MEDLINE=93359075; PubMed=8394834;
RA Morrow J.A., Lutz E.M., West K.M., Fink G., Harmar A.J.;
RT "Molecular cloning and expression of a cDNA encoding a receptor for
RL pituitary adenylate cyclase activating polypeptide (PACAP).";
FEBS Lett. 329:99-105(1993).
RN [6]
RP SEQUENCE OF 115-523 FROM N.A.
RC STRAIN=Wistar;
RA Svoboda M., Ciccarelli E., Tastenoy M., Christophe J.;
RA Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,
CC LUTEALIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND
CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM
CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE
CC GASTROINTESTINAL TRACT.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=HIP-HOP1;
CC IsoId=P32215-1; Sequence=Displayed;
CC Name=HOP1;
CC IsoId=P32215-2; Sequence=VSP_002005, VSP_002006;
CC Name=HOP2;
CC IsoId=P32215-3; Sequence=VSP_002005, VSP_002007;
CC Name=HIP;
CC IsoId=P32215-4; Sequence=VSP_002008;
CC Name=PACAP-R;
CC IsoId=P32215-5; Sequence=VSP_002009;

```

```
CC CC -!- TISSUE SPECIFICITY: HYPOTHALAMUS, ANTERIOR PITUITARY, ADRENAL
CC CC MEDULLA, TESTICULAR GERM CELLS.
CC CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC CC -----
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CC CC -----
CC CC EMBL; D16465; BAA03932.1; -
CC CC EMBL; D16680; AAA41792.1; -
CC CC EMBL; D14908; BAA03608.1; -
CC CC EMBL; D14909; BAA03609.1; -
CC CC EMBL; D23272; CAA80810.1; -
CC CC EMBL; D23273; CAA80811.1; -
CC CC EMBL; D23274; CAA80812.1; -
CC CC EMBL; D23275; CAA80813.1; -
CC CC EMBL; D23279; CAA80817.1; -
CC CC EMBL; D23282; CAA80821.1; -
CC CC EMBL; D23282; CAA80820.1; -
CC CC EMBL; D16506; AAA02990.1; -
CC CC EMBL; D22735; CAA80429.1; -
CC CC PIR; JN0616; JN0616.
CC CC PIR; S36114; S36114.
CC CC PIR; S39060; S39060.
CC CC PIR; S39061; S39061.
CC CC PIR; S39061; S39061.
CC CC InterPro; IPR000832; GPCR_secretin.
CC CC Pfam; PF00002; 7tm_2; 1.
CC CC Pfam; PF02793; HRM; 1.
CC CC PRINTS; PR00249; GPCRSECRETIN.
CC CC SMART; SM00008; Hormr; 1.
CC CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
CC CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
CC CC PROSITE; PS00650; G_PROTEIN_RECP_F2_3; 1.
CC CC PROSITE; PS00650; G_PROTEIN_RECP_F2_4; 1.
CC CC PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
CC CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC CC Spermatogenesis; Alternative splicing.
CC CC SIGNAL 1 19
CC CC CHAIN 20 523
CC CC PITUITARY ADENYLATE CYCLASE ACTIVATING
CC CC POLYPEPTIDE TYPE IA RECEPTOR.
CC CC EXTRACELLULAR (POTENTIAL).
CC CC 1 (POTENTIAL).
CC CC 2 (POTENTIAL).
CC CC 3 (POTENTIAL).
CC CC 4 (POTENTIAL).
CC CC 5 (POTENTIAL).
CC CC 6 (POTENTIAL).
CC CC 7 (POTENTIAL).
CC CC CYTOPLASMIC (POTENTIAL).
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC L -> F (in isoform HOP1 and isoform
CC CC HOP2).
CC CC /FTid=VSP_002005.
CC CC Missing (in isoform HOP1).
CC CC /FTid=VSP_002006.
CC CC Missing (in isoform HOP2).
CC CC /FTid=VSP_002007.
CC CC Missing (in isoform HIP).
CC CC /FTid=VSP_002008.
CC CC Missing (in isoform PACAP-R).
CC CC /FTid=VSP_002009.
CC CC -----
```

```
FT CONFLICT 449 449 F -> L (IN REF. 1).
FT CONFLICT 510 511 QL -> HV (IN REF. 6).
FT CONFLICT 516 516 SL -> TV (IN REF. 6).
SQ SEQUENCE 523 AA; 59637 MW; 038CA413ED37E44 CRC64;

Query Match
Best Local Similarity 1.78; Score 9; DB 1; Length 523;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 LFVSFMLRA 191
| | | | |
Db 191 LFVSFMLRA 199

RESULT 35
PT25_STYPL STANDARD; PRT; 117 AA.
AC P28217;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Protein-tyrosine phosphatase 25 (EC 3.1.3.48) (Fragment).
GN STY 25.
OS Styela plicata (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7726;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139172; PubMed=1704870;
RA Matthews R.J., Flores E., Thomas M.L.;
RT "Protein tyrosine phosphatase domains from the protochordate Styela
RT plicata.";
RL Immunogenetics 33:33-41(1991).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -----
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CC -----
CC EMBL; M38010; AAA29843.1; -
CC HSSP; P29350; ICWZ.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; TYR_PP.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; PARTIAL.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; PARTIAL.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
CC Hydrolase.
CC FT NON TER 1 1
CC FT NON TER 117 117
SQ SEQUENCE 117 AA; 13422 MW; 9CAE0F5D70B7EF28 CRC64;

Query Match
Best Local Similarity 1.58; Score 8; DB 1; Length 117;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 449 GSVLTITVT 456
| | | | |
Db 69 GSVLTITVT 76

RESULT 36
CRF2_HUMAN STANDARD; PRT; 411 AA.
AC Q13324; O43461; Q99431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
```

28-FEB-2003 (Rel. 41, Last annotation update)
Corticotropin releasing factor receptor 2 precursor (CRF-R 2) (CRF2)
(Corticotropin-releasing hormone receptor 2) (CRH-R 2).
CRH2R OR CRF2R
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM CRF2-ALPHA).
MEDLINE=96107120; PubMed=8536644;
Liu C.W., Lovenberg T.W., Barry G., Oltersdorf T., Grigoriadis D.E.,
de Souza E.B.;
"Cloning and characterization of the human corticotropin-releasing
factor-2 receptor complementary deoxyribonucleic acid.";
Endocrinology 137:72-77(1996).
[2]
SEQUENCE FROM N.A. (ISOFORM CRF2-BETA).
TISSUE=Amgdala;
Kostich W.A., Chen A., Sperle K., Horlick R.A., Patterson J.,
Hyde T.M., Largent B.L.;
"Molecular cloning of the human CRH2B receptor isoform: divergence
from the rodent isoform in sequence and expression pattern.";
Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A. (ISOFORM CRF2-GAMMA).
TISSUE=Amgdala;
MEDLINE=96381934; PubMed=9717834;
Kostich W.A., Chen A., Sperle K., Largent B.L.;
"Molecular identification and analysis of a novel human corticotropin-
releasing factor (CRF) receptor: the CRF2gamma receptor.";
Mol. Endocrinol. 12:1077-1085(1998).
[4]
SEQUENCE FROM N.A. (ISOFORMS CRF2-ALPHA AND CRF2-GAMMA).
Andrews S., Langston Y., Stoneking T., Maupin R.;
Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A. (ISOFORM CRF2-ALPHA).
Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
receptor genes.";
Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE OF 1-88 FROM N.A. (ISOFORM CRF2-BETA).
TISSUE=Skeletal muscle;
MEDLINE=97342544; PubMed=9199241;
Valdenaire O., Giller T., Breu V., Gottowik J., Kilpatrick G.;
"A new functional isoform of the human CRF2 receptor for
corticotropin-releasing factor.";
Biochim. Biophys. Acta 1352:129-132(1997).
-!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
III. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
ACTIVATE ADENYL CYCLASE.
-!- SUBCELLULAR LOCATION: integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=3;
Name=CRF2-alpha;
IsoId=Q13324-1; Sequence=Displayed;
Name=CRF2-beta;
IsoId=Q13324-2; Sequence=VSP_001999;
Name=CRF2-gamma;
IsoId=Q13324-3; Sequence=VSP_002000;
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL; U34587; AA91320.1; -;
DR EMBL; AF011406; AAB94503.1; -;
DR EMBL; AF019381; AAB94562.1; -;
DR EMBL; AC004976; AAC71653.1; -;
DR EMBL; AC004976; AAC71654.1; -;
DR EMBL; AB065699; BAC05922.1; -;
DR EMBL; Y10151; CAA71235.1; -;
DR Genew; HGNC:2358; CRHR2.
DR MIM; 602034; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0015056; P:corticotropin-releasing factor receptor ac. .; TAS.
DR GO; GO:0007188; P:G-protein signaling, coupled to CAMP nucleo. .; TAS.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; HormR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02027; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS02027; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS02027; G_PROTEIN_RECEP_F2_5; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Alternative splicing.
FT SIGNAL 1 17
FT CHAIN 18 411
FT POTENTIAL.
CORTICOTROPIN RELEASING FACTOR RECEPTOR
2.
FT DOMAIN 18 118
EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 139
1 (POTENTIAL).
FT DOMAIN 140 148
CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 168
2 (POTENTIAL).
FT DOMAIN 169 185
EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 186 209
3 (POTENTIAL).
FT DOMAIN 210 223
CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 245
4 (POTENTIAL).
FT DOMAIN 246 264
EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 265 287
5 (POTENTIAL).
FT DOMAIN 288 310
CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 311 330
6 (POTENTIAL).
FT DOMAIN 331 345
EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 346 365
7 (POTENTIAL).
FT DOMAIN 366 411
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 41 41
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 74 74
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 86 86
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 94 94
MDALLSHLSLSEANSLALAEELLDDGWGPPDPE -> MGR
PSGPPGLDVIYVPHLLLCCLLPPLPPLQYAAQSQMPKQPLW
ALLEQYCHYCHTINTLNLS (in isoform CRF2-beta).
/FTId=VSP_001999.
MDALLSHLSLSEANSLALAEELLDDGWGPPDPE -> MGR
EPMPEDRLGFPQLFCQ (in isoform
CRF2-gamma).
/FTId=VSP_002000.
R -> H (IN REF. 1).
FT CONFLICT 185 185
FT SEQUENCE 411 AA; 47687 MW; 96B99A93594CF07F CRC64;
SQ
Query Match 1.5%; Score 8; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 403 SFQGFVVS 410
|||||||
DB 349 SFQGFVVS 356
RESULT 37
ID_CRF2_RAT
AC P47866; STANDARD; PRT; 411 AA.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

FT	TRANSEM	348	367	7 (POTENTIAL).
FT	DOMAIN	368	413	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	16	16	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	77	77	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	89	89	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	97	97	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	413 AA; 48458 MW; DAD422FOA96C4626 CRC64;		

Query Match 1.5%; Score 8; DB 1; Length 413;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	403 SFQGFVVS	410
Db	351 SFQGFVVS	358

RESULT 40

CRF1_MOUSE	STANDARD;	PRT;	415 AA.
ID	CRF1_MOUSE		
AC	P35347;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)		
DE	(Corticotropin-releasing hormone receptor 1) (CRH-R 1).		
DE	CRHR1 OR CRHR.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Pituitary;		
RX	MEDLINE=94063063; PubMed=8243652;		
RA	Vita N., Laurent P., Lefort S., Chalou P., Lelias J.-M., Kaghad M.,		
RA	le Fur G., Caput D., Ferrara P.;		
RT	"Primary structure and functional expression of mouse pituitary and		
RT	human brain corticotropin releasing factor receptors.";		
RL	FEBS Lett. 335:1-5(1993).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ILS, and ISS;		
RX	MEDLINE=21363810; PubMed=11471062;		
RA	Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,		
RA	Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;		
RT	"High-throughput sequence identification of gene coding variants		
RT	within alcohol-related QTLs.";		
RL	Mamm. Genome 12:657-663(2001).		
CC	-1- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.		
CC	SHOWS HIGH-AFFINITY CRF BINDING. THE ACTIVITY OF THIS RECEPTOR IS		
CC	MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: BRAIN, PITUITARY GLAND, TESTIS. NOT DETECTED		
CC	IN PLACENTA, PERIPHERAL BLOOD, LYMPHOCYTES, KIDNEY AND LIVER.		
CC	-1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; X72305; CAA51053.1; -;		
DR	EMBL; AF483484; AAL90758.1; -;		
DR	EMBL; AF483485; AAL90759.1; -;		
DR	PIR; S39535; S39535.		
DR	MGI; MGI:88498; Crhr1.		
DR	InterPro; IPR000832; GPCR secretin.		
DR	InterPro; IPR001879; horrm receptor.		


```

FT DOMAIN 214 227 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 228 249 4 (POTENTIAL).
FT DOMAIN 250 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 269 291 5 (POTENTIAL).
FT DOMAIN 292 314 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 315 334 6 (POTENTIAL).
FT DOMAIN 335 349 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 350 369 7 (POTENTIAL).
FT DOMAIN 370 415 CYTOPLASMIC (POTENTIAL).
FT DISULFID 30 54
FT DISULFID 44 87
FT DISULFID 68 102
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .)
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .)
FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .)
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .)
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .)
SQ SEQUENCE 415 AA; 47842 MW; 48D6704B31D4C013 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 415;
Best Local Similarity 100.0%; Pred.No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
DB 353 SFQGFVVS 360
|||||

RESULT 42
CRF1_SHEEP STANDARD; PRT; 415 AA.
AC Q62772;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
GN CRHR1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=pituitary;
RX MEDLINE=99079328; PubMed=9863624;
RA Myers D.A., Trinh J.V., Myers T.R.;
RT "Structure and function of the ovine type 1 corticotropin releasing
factor receptor (CRF1) and a carboxyl-terminal variant.";
RL Mol. Cell. Endocrinol. 144:21-35(1998).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
CC SHOWS HIGH-AFFINITY CRF BINDING. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AF054582; AAC08027.1; -
CC InterPro; IPR000832; GPCR secretin.
CC InterPro; IPR01879; hormn_receptor.
CC Pfam; PF00002; 7tm 2; 1.
CC Pfam; PF02793; HRM1; 1
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; HormR; 1.

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DR PROSITE; PS00649; G PROTEIN RECEPTOR F2.1; FALSE_NEG.
DR PROSITE; PS00650; G PROTEIN RECEPTOR F2.2; 1.
DR PROSITE; PS00651; G PROTEIN RECEPTOR F2.3; 1.
DR PROSITE; PS00652; G PROTEIN RECEPTOR F2.4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Phosphorylation.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 415 CORTICOTROPIN RELEASING FACTOR RECEPTOR
1.
FT DOMAIN 24 121 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 122 142 1 (POTENTIAL).
FT DOMAIN 143 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 171 2 (POTENTIAL).
FT DOMAIN 172 189 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 190 213 3 (POTENTIAL).
FT DOMAIN 214 227 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 228 249 4 (POTENTIAL).
FT DOMAIN 250 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 269 291 5 (POTENTIAL).
FT DOMAIN 292 314 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 315 334 6 (POTENTIAL).
FT DOMAIN 335 349 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 350 369 7 (POTENTIAL).
FT DOMAIN 370 415 CYTOPLASMIC (POTENTIAL).
FT DISULFID 30 54 BY SIMILARITY.
FT DISULFID 44 87 BY SIMILARITY.
FT DISULFID 68 102 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 415 AA; 47558 MW; FAS652D12B4CDC4 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 415;
Best Local Similarity 100.0%; Pred.No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
DB 353 SFQGFVVS 360
|||||

RESULT 43
CRF1_XENLA STANDARD; PRT; 415 AA.
AC Q42602;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
GN CRF1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97465573; PubMed=9326293;
RA Dautzenberg F.M., Dietrich K., Palchaudhuri M.R., Spiess J.;
RT "Identification of two corticotropin-releasing factor receptors from
RT Xenopus laevis with high ligand selectivity: unusual pharmacology of
RT the type 1 receptor.";
RL J. Neurochem. 69:1640-1649(1997).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
CC SHOWS HIGH-AFFINITY BINDING FOR UROTENSIN I. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
CC CYCLASE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

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CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y14036; CAA74363.1; -.
CC InterPro; IPR000832; GPCR_secretin.
CC Pfam; PF00002; 7tm.2; 1.
CC PRINTS; PF02793; HRM; 1.
CC SMART; SM00008; HORMR; 1.
CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
CC PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
CC PROSITE; PS50261; G_PROTEIN_RECP_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 24
FT CHAIN 25 415
FT DOMAIN 25 121
FT TRANSMEM 122 142
FT DOMAIN 143 151
FT TRANSMEM 152 171
FT DOMAIN 172 189
FT TRANSMEM 190 213
FT DOMAIN 214 227
FT TRANSMEM 228 249
FT DOMAIN 250 268
FT TRANSMEM 269 291
FT DOMAIN 292 314
FT TRANSMEM 315 334
FT DOMAIN 335 349
FT TRANSMEM 350 369
FT DOMAIN 370 415
FT DISULFID 30 54
FT DISULFID 44 87
FT CARBOHYD 68 102
FT CARBOHYD 38 38
FT CARBOHYD 45 45
FT CARBOHYD 78 78
FT CARBOHYD 90 90
SQ SEQUENCE 415 AA; 47786 MW; 74ED24C17907B74D CRC64;

Query Match 1.5%; Score 8; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 SFQGFVVS 410
Db 353 SFQGFVVS 360
|||||

RESULT 44
ID_CRF1_CHICK STANDARD; PRT; 420 AA.
AC Q90812;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE Corticotropin-releasing hormone receptor 1 (CRH-R 1).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]

```

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RP SEQUENCE FROM N.A.
RX MEDLINE=96107136; PubMed=8536612;
RA Yu J., Xie L.Y.; Abou-Samra A.-B.;
RT "Molecular cloning of a type A chicken corticotropin-releasing factor
RT receptor with high affinity for urotensin I.";
RL Endocrinology 137:192-197(1996).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
CC SHOWS HIGH-AFFINITY BINDING FOR UROTENSIN I. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L41563; AAA96656.1; -.
CC InterPro; IPR000832; GPCR_secretin.
CC Pfam; PF00002; 7tm.2; 1.
CC PRINTS; PF02793; HRM; 1.
CC SMART; SM00008; HORMR; 1.
CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
CC PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
CC PROSITE; PS50261; G_PROTEIN_RECP_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 28
FT CHAIN 29 420
FT DOMAIN 29 126
FT TRANSMEM 127 147
FT DOMAIN 148 156
FT TRANSMEM 157 176
FT DOMAIN 177 194
FT TRANSMEM 195 218
FT DOMAIN 219 232
FT TRANSMEM 233 254
FT DOMAIN 255 273
FT TRANSMEM 274 296
FT DOMAIN 297 319
FT TRANSMEM 320 339
FT DOMAIN 340 354
FT TRANSMEM 355 374
FT DOMAIN 375 420
FT DISULFID 35 59
FT DISULFID 49 92
FT DISULFID 73 107
FT CARBOHYD 43 43
FT CARBOHYD 50 50
FT CARBOHYD 83 83
FT CARBOHYD 95 95
FT CARBOHYD 103 103
SQ SEQUENCE 420 AA; 48600 MW; 8C5C992925F62316 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 420;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 SFQGFVVS 410
Db 358 SFQGFVVS 365
|||||

RESULT 45
ID_CRF2_MOUSE STANDARD; PRT; 431 AA.

```


RN [3] SEQUENCE FROM N.A.
 RA Sakai K., Yamada M., Horiba N., Wakui M., Demura H., Suda T.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM CRF-R3).
 RC TISSUE=Hippocampus;
 RX MEDLINE=95110332; PubMed=7811272;
 RA Ross P.C., Kostas C.M., Ramabhadran T.V.;
 RT "A variant of the human corticotropin-releasing factor (CRF)
 RL receptor: cloning, expression and pharmacology";
 RL Biochem. Biophys. Res. Commun. 205:1836-1842(1994).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM CRF-R4).
 RX MEDLINE=20065650; PubMed=10598591;
 RA Grammatopoulos D.K., Dai Y., Randeve H.S., Levine M.A., Karteris E.,
 RA Easton A.J., Hillhouse E.W.;
 RT "A novel spliced variant of the type 1 corticotropin-releasing hormone
 RT receptor with a deletion in the seventh transmembrane domain present
 RT in the human pregnant term myometrium and fetal membranes.";
 RL Mol. Endocrinol. 13:2189-2202(1999).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
 CC SHOWS HIGH-AFFINITY CRF BINDING. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=CRF-R1;
 CC IsoId=P34998-1; Sequence=Displayed;
 CC Name=CRF-R2;
 CC IsoId=P34998-2; Sequence=VSP_001997;
 CC Name=CRF-R3;
 CC IsoId=P34998-3; Sequence=VSP_001996, VSP_001997;
 CC Note=Does not bind to CRF with high affinity;
 CC Name=CRF-R4; Synonyms=ID;
 CC IsoId=P34998-4; Sequence=VSP_001997, VSP_001998;
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE CEREBELLUM,
 CC PITUITARY, CEREBRAL CORTEX AND OLFACTORY LOBE.
 CC -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; L23333; AAA35719.1; -.
 DR EMBL; L23332; AAA35718.1; -.
 DR EMBL; X72304; CAA51052.1; -.
 DR EMBL; AF039523; AAC69993.1; JOINED.
 DR EMBL; AF039510; AAC69993.1; JOINED.
 DR EMBL; AF039511; AAC69993.1; JOINED.
 DR EMBL; AF039512; AAC69993.1; JOINED.
 DR EMBL; AF039513; AAC69993.1; JOINED.
 DR EMBL; AF039514; AAC69993.1; JOINED.
 DR EMBL; AF039515; AAC69993.1; JOINED.
 DR EMBL; AF039516; AAC69993.1; JOINED.
 DR EMBL; AF039517; AAC69993.1; JOINED.
 DR EMBL; AF039518; AAC69993.1; JOINED.
 DR EMBL; AF039519; AAC69993.1; JOINED.
 DR EMBL; AF039520; AAC69993.1; JOINED.
 DR EMBL; AF039521; AAC69993.1; JOINED.
 DR EMBL; AF039522; AAC69993.1; JOINED.
 DR EMBL; U16273; AAC50073.1; -.
 DR EMBL; AF180301; AAD52688.1; -.
 DR PIR; I38879; I38879.
 DR PIR; I60975; A48260.
 DR Genew; HGNC:2357; CRHR1.
 DR MIM; 122561; -.

DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0015056; F: corticotropin-releasing factor receptor ac. .; TAS.
 DR GO; GO:0007190; P: adenylate cyclase activation; TAS.
 DR GO; GO:0007188; P: G-protein signaling, coupled to CAMP nucleo. .; TAS.
 DR GO; GO:0006955; P: immune response; TAS.
 DR GO; GO:0007567; P: parturition; TAS.
 DR InterPro; IPR000832; GPCR_receptor.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm.2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HORMR; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Phosphorylation; Alternative splicing.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 444 CORTICOTROPIN RELEASING FACTOR RECEPTOR
 FT 1.
 FT DOMAIN 24 121 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 122 142 1 (POTENTIAL).
 FT DOMAIN 143 180 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 181 200 2 (POTENTIAL).
 FT DOMAIN 201 218 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 219 242 3 (POTENTIAL).
 FT DOMAIN 243 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 278 4 (POTENTIAL).
 FT DOMAIN 279 297 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 298 320 5 (POTENTIAL).
 FT DOMAIN 321 343 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 344 363 6 (POTENTIAL).
 FT DOMAIN 364 378 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 379 398 7 (POTENTIAL).
 FT DOMAIN 399 444 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 30 54 BY SIMILARITY.
 FT DISULFID 44 87 BY SIMILARITY.
 FT DISULFID 68 102 BY SIMILARITY.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 90 98 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 41 81 GLCNASVDLIGTCWSPAGQVVRPCPAFFYGVYNTTN
 -> D (in isoform CRF-R3).
 /FTid=VSP_001996.
 FT VARSPLIC 146 174 Missing (in isoform CRF-R2, isoform
 CRF-R3 and isoform CRF-R4).
 /FTid=VSP_001997.
 FT VARSPLIC 385 398 Missing (in isoform CRF-R4).
 /FTid=VSP_001998.
 SQ SEQUENCE 444 AA; 50719 MW; 7221AEFB0E7AA8ED CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 444;
 Best Local Similarity 100.0%; Pred.No. 6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 403 SFQGFVVS 410
 |||||
 Db 382 SFQGFVVS 389
 RESULT 47
 FCY2 YEAST
 ID FCY2 YEAST STANDARD; PRT; 533 AA.
 AC F17064;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DR Purine-cytosine permease (PCP) (Cytosine/purine transport protein).
 GN FCY2 OR YER056C.
 OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 28583 / FL100;
 RX MEDLINE=90279501; PubMed=2191181;
 RA Weber E., Rodriguez C., Chevalier M.R., Jund R.;
 RT "The purine-cytosine permease gene of *Saccharomyces cerevisiae*:
 RT primary structure and deduced protein sequence of the PCY2 gene
 RT product.";
 RL Mol. Microbiol. 4:585-596(1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX PubMed=9169868;
 RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
 RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
 RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
 RA Hunnicke-Smith S., Hymen R.W., Kayser A., Komp C., Lashkari D., Lew H.,
 RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
 RA Oh C., Patel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
 RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome V";
 RL Nature 397:78-81(1997).
 RN [3]
 RN SEQUENCE OF 380-533 FROM N.A.
 RC MEDLINE=83161150; PubMed=6300123;
 RA Hinnebusch A.G., Fink G.R.;
 RT "Repeated DNA sequences upstream from HIS1 also occur at several
 RT other co-regulated genes in *Saccharomyces cerevisiae*.";
 RL J. Biol. Chem. 258:5238-5247(1983).
 RN [4]
 RN MUTAGENESIS.
 RP MEDLINE=95282509; PubMed=7762297;
 RA Rodriguez C., Bloch J.C., Chevalier M.R.;
 RT "The immunodetected yeast purine-cytosine permease is not N-linked
 RT glycosylated, nor are glycosylation sequences required to have a
 RT functional permease.";
 RL Yeast 11:15-23(1995).
 CC -1- FUNCTION: THIS PERMEASE HAS A BROAD SPECIFICITY TOWARDS PURINES,
 CC AND ALSO TRANSPORT CYTOSINE AND 5-METHYLCYTOSINE BUT NEITHER
 CC URACIL NOR THYMINE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: NOT N-GLYCOSYLATED.
 CC -1- SIMILARITY: TO YEAST PCY21 AND YGL186C.
 CC -----
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 CC -----
 DR EMBL; X51751; CAA36040.1; -;
 DR EMBL; U18813; BAB64592.1; -;
 DR EMBL; V01306; -; NOT ANNOTATED_CDS.
 DR PIR; S50559; GREYCP.
 DR SGD; S0000858; PCY2.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR GO; GO:0015392; F:cytosine-purine permease activity; IDA.
 DR GO; GO:0015856; P:cytosine transport; IDA.
 DR GO; GO:0006863; P:purine transport; IDA.
 DR InterPro; IPR001248; Cyt_pur_permease.
 DR Pfam; PF02133; Transp_cyt_pur; 1.
 DR TIGRfams; TIGR00800; ncsl; 1.
 DR Transmembrane.
 KW TRANSMEM 99 119 POTENTIAL.
 FT TRANSMEM 122 141 POTENTIAL.
 FT DOMAIN 165 184 SURFACE SEEKING (POTENTIAL).
 FT TRANSMEM 199 218 POTENTIAL.
 FT TRANSMEM 257 276 POTENTIAL.

FT TRANSMEM 301 320 POTENTIAL.
 FT TRANSMEM 348 367 POTENTIAL.
 FT TRANSMEM 399 418 POTENTIAL.
 FT TRANSMEM 466 485 POTENTIAL.
 FT TRANSMEM 192 192 V -> M (IN REF. 1).
 FT TRANSMEM 261 261 A -> G (IN REF. 1).
 FT TRANSMEM 459 459 D -> Y (IN REF. 3).
 SQ SEQUENCE 533 AA; 58201 MW; 762DDB9483A546AC CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 533;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 264 LIFVAFPS 271
 DB 133 LIFVAFPS 140
 RESULT 48
 HFQ AGRTS STANDARD; PRT; 80 AA.
 ID HFQ AGRTS
 AC Q8UF88;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE HFQ protein.
 GN HFQ OR ATU1450 OR AGR_C_2673.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*
 RT C58.";
 RL Science 294:2317-2323(2001).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmel K., Gordon J., Vaubin M., Lartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 CC -1- FUNCTION: RNA-binding protein that stimulates the elongation of
 CC poly(A) tails (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE HFQ FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; AE009105; ALA42456.1; -;
 DR EMBL; AE008070; -; NOT ANNOTATED_CDS.

Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 VGYSISF 156
 |||||
Db 153 VGYSISF 159

Search completed: December 9, 2003, 09:01:13
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2003, 08:57:00 ; Search time 40 Seconds

(without alignments)
3490.161 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAMLGASLHWGMLGLSCL.....DDILMEKPSRPMESNPDTG 541

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- 1: SP_TREMBL_23:*
- 2: SP_bacteria:*
- 3: SP_fungi:*
- 4: SP_human:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_nhc:*
- 8: SP_organelle:*
- 9: SP_phage:*
- 10: SP_plant:*
- 11: SP_rodent:*
- 12: SP_virus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*
- 15: SP_rvirus:*
- 16: SP_bacteriap:*
- 17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	363	67.1	621	4 Q8N429	Q8N429 homo sapien
2	38	7.0	169	11 Q9R1D4	Q9R1D4 mus musculus
3	38	7.0	237	11 Q8BUM8	Q8BUM8 mus musculus
4	38	7.0	546	11 Q91V95	Q91V95 mus musculus
5	27	5.0	575	13 Q9PWB7	Q9PWB7 brachydanio
6	20	3.7	94	13 Q9PRG1	Q9PRG1 ictalurus p
7	19	3.5	528	4 Q81V17	Q81V17 homo sapien
8	18	3.3	333	4 Q8N5V1	Q8N5V1 homo sapien
9	18	3.3	536	13 Q9PVD3	Q9PVD3 brachydanio
10	18	3.3	591	11 Q91WV4	Q91WV4 mus musculus
11	18	3.3	595	6 Q9TU31	Q9TU31 canis famil
12	18	3.3	964	4 Q8NHB4	Q8NHB4 homo sapien
13	16	3.0	419	13 Q8AXV3	Q8AXV3 fugu rubrip
14	13	2.4	418	13 Q91B32	Q91B32 gallus gall
15	13	2.4	444	13 Q9YHC6	Q9YHC6 rana ridibu
16	13	2.4	459	11 Q9J140	Q9J140 mus musculus

17	11	2.0	542	13 Q9PVD2	Q9PVD2 brachydanio
18	10	1.8	48	11 Q9J1Y4	Q9J1Y4 mus musculus
19	10	1.8	167	13 Q9YHC8	Q9YHC8 rana ridibu
20	10	1.8	227	4 Q8WUR8	Q8WUR8 homo sapien
21	9	1.7	91	13 Q98TU4	Q98TU4 brachydanio
22	9	1.7	202	13 Q98955	Q98955 meleagris g
23	9	1.7	374	6 Q8WME0	Q8WME0 ovis aries
24	9	1.7	402	6 Q8WQ99	Q8WQ99 ovis aries
25	9	1.7	419	13 Q8AXV4	Q8AXV4 fugu rubrip
26	9	1.7	459	11 Q8BGA4	Q8BGA4 mus musculus
27	9	1.7	465	13 Q73769	Q73769 carassius a
28	9	1.7	485	11 Q8KOB5	Q8KOB5 mus musculus
29	9	1.7	495	11 Q8BLT3	Q8BLT3 mus musculus
30	9	1.7	589	6 Q9GMD1	Q9GMD1 cryptolegus
31	8	1.5	37	4 Q8WXR5	Q8WXR5 homo sapien
32	8	1.5	126	13 Q57671	Q57671 meleagris g
33	8	1.5	168	13 Q9YHC7	Q9YHC7 rana ridibu
34	8	1.5	304	11 Q8BM22	Q8BM22 mus musculus
35	8	1.5	379	2 Q8RM00	Q8RM00 acinetobact
36	8	1.5	405	13 Q98UC1	Q98UC1 ameiturus ne
37	8	1.5	410	6 Q8WML9	Q8WML9 tupaia bela
38	8	1.5	414	13 Q8AWA1	Q8AWA1 oncorhynch
39	8	1.5	415	6 Q9BGU4	Q9BGU4 bos taurus
40	8	1.5	415	6 Q8WMM0	Q8WMM0 tupaia bela
41	8	1.5	415	11 Q8K3R2	Q8K3R2 mesocricetu
42	8	1.5	428	13 Q98UC0	Q98UC0 ameiturus ne
43	8	1.5	430	13 Q8AWA2	Q8AWA2 oncorhynch
44	8	1.5	437	6 Q8WML8	Q8WML8 tupaia bela
45	8	1.5	438	13 Q73768	Q73768 carassius a

ALIGNMENTS

RESULT 1

Q8N429	Q8N429	PRELIMINARY;	PRT;	621 AA.
AC	Q8N429			
DT	01-OCT-2002 (Tremblrel. 22, Created)			
DT	01-OCT-2002 (Tremblrel. 23, Last sequence update)			
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)			
DB	Parathyroid hormone receptor 2 (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Strausberg R.;			
RL	Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC036811; AAH36811.1; -			
DR	InterPro; IPR000832; GPCR_secretin.			
DR	InterPro; IPR001879; hormn_receptor.			
DR	Pfam; PF00002; 7tm_2; 1.			
DR	Pfam; PF02793; HRM; 1.			
DR	PRINTS; PR00249; GPCRSECRETIN.			
DR	SMART; SM00008; HORMR; 1.			
DR	PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.			
DR	PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.			
DR	PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.			
DR	PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.			
KW	Receptor.			
FT	NON TER			
SQ	SEQUENCE 621 AA; 69299 MW; 880A5A84889436D2 CRC64;			

Query Match 67.1%; Score 363; DB 4; Length 621;
Best Local Similarity 99.8%; Pred.No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	4	LGASLHWGMLGLSCLLARAQLDSGTITIEQIVLVKAKVOCNELNTAQLEGEGNC	63
Db	75	LGASLHWGMLGLSCLLARAQLDSGTITIEQIVLVKAKVOCNELNTAQLEGEGNC	134

QY 64 FPEWDLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTWNYS 123
DB 135 FPEWDLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTWNYS 194
QY 124 DCLRFLOPDISIGKQEPFRLYVMTYVGSISFGSLAVALIIGYFRLHCTRNVIHML 183
DB 195 DCLRFLOPDISIGKQEPFRLYVMTYVGSISFGSLAVALIIGYFRLHCTRNVIHML 254
QY 184 FVSFMLRATSIIVKDRVVAHIGVKELSLIMQDDPQNSIEATSDKSYIGCKIAYVWF 243
DB 255 FVSFMLRATSIIVKDRVVAHIGVKELSLIMQDDPQNSIEATSDKSYIGCKIAYVWF 314
QY 244 IYFLATNYWIIIVLVEGLHNLIFVAFSDTKYLGWFFILGWGFPFAAFVAAVARATLAD 303
DB 315 IYFLATNYWIIIVLVEGLHNLIFVAFSDTKYLGWFFILGWGFPFAAFVAAVARATLAD 374
QY 304 ARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRKLAK 363
DB 375 ARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRKLAK 434
QY 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRMHCBELFNSFGFFVSIYCYCNGEVOAE 423
DB 435 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRMHCBELFNSFGFFVSIYCYCNGEVOAE 494
QY 424 VKKMSRWNLSDVWKRTTPCGSRRCGSLVLTTHSTSSQSQVAA 467
DB 495 VKKMSRWNLSDVWKRTTPCGSRRCGSLVLTTHSTSSQSQVAA 538

RESULT 2
Q9R1D4
ID Q9R1D4 PRELIMINARY; PRT; 169 AA.
AC Q9R1D4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Parathyroid hormone type-2 receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC TISSUE=Brain;
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
parathyroid hormone and not by human or teleost parathyroid hormone-
related peptide. Implications for the evolutionary conservation of
calcium-regulating peptide hormones.";
RL J. Biol. Chem. 274:23035-23042(1999).
DR EMBL; AF132083; AAD51909.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS50261; G_PROTEIN_RECEPTOR_F2_4; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 169
SQ SEQUENCE 169 AA; 19674 MW; 748CC8231F1C69EA CRC64;

Query Match 7.0%; Score 38; DB 11; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.9e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILFNTVRLATKIWETNAVGH 353
DB 66 WIYQAPILAAIGLNFILFNTVRLATKIWETNAVGH 103

RESULT 3
Q8BUM8

ID Q8BUM8 PRELIMINARY; PRT; 237 AA.
AC Q8BUM8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Parathyroid hormone receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK083278; BAC38840.1; -.
FT NON_TER 1
SQ SEQUENCE 237 AA; 26863 MW; FA35AC19C1FF5257 CRC64;

Query Match 7.0%; Score 38; DB 11; Length 237;
Best Local Similarity 100.0%; Pred. No. 3.9e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILFNTVRLATKIWETNAVGH 353
DB 4 WIYQAPILAAIGLNFILFNTVRLATKIWETNAVGH 41

RESULT 4
Q91V95
ID Q91V95 PRELIMINARY; PRT; 546 AA.
AC Q91V95;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Parathyroid hormone receptor.
GN PTHR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=ILS, and ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-Throughput Sequence Identification of Gene Coding Variants
Within Alcohol-Related QTLs.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF332078; AAK56106.1; -.
DR EMBL; AF332077; AAK56105.1; -.
DR EMBL; AK045576; BAC32420.1; -.
DR MGD; MGI:2180917; Pthr2.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEPTOR_F2_1; 1.


```
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to parathyroid hormone receptor 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RA Strausberg R.;
PL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031578; AAH31578.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 333 AA; 37588 MW; B176DBBASC6A68E4 CRC64;

Query Match 3.3%; Score 18; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
   |||||
DB 290 YFLATNYWILVEGLYLH 307

RESULT 9
Q9PVD3 PRELIMINARY; PRT; 536 AA.
AC Q9PVD3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone receptor PTH1R.
GN PTH1R.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99428481; PubMed=10497171;
RA Rubin D.A., Juppner H.;
RT "Zebrafish express the common parathyroid hormone/parathyroid hormone-
RT related peptide receptor (PTH1R) and a novel receptor (PTH3R) that is
RT preferentially activated by mammalian and fuguish parathyroid
RT hormone-related peptide."
RL J. Biol. Chem. 274:28185-28190(1999).
DR EMBL; AF132084; AAF01265.1; -.
DR HSP; Q03431; 1BL1.
DR ZFIN; ZDB-GENE-991123-8; pthrl.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 536 AA; 61454 MW; 653B0A56DB2C9FA9 CRC64;
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Query Match 3.3%; Score 18; DB 13; Length 536;
Best Local Similarity 100.0%; Pred. No. 9.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRYIHMLF 184
   |||||
DB 167 GYFRLHCTRYIHMLF 184

RESULT 10
Q91WV4 PRELIMINARY; PRT; 591 AA.
AC Q91WV4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Parathyroid hormone receptor.
GN PTHR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013446; AAH13446.1; -.
DR MGD; MGI:97801; Pthr.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 591 AA; 66361 MW; 6E29CF63B5BAFEED CRC64;

Query Match 3.3%; Score 18; DB 11; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
   |||||
DB 290 YFLATNYWILVEGLYLH 307

RESULT 11
Q9TU31 PRELIMINARY; PRT; 595 AA.
AC Q9TU31;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Parathyroid hormone receptor-1.
GN PTH1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
RT "Molecular cloning and functional characterization of the canine
RT parathyroid hormone receptor-1 (PTH1)."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167095; AAD55938.1; -.
DR HSP; Q03431; 1BL1.
```

DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 595 AA; 66308 MW; 09568ECF38D4D258 CRC64;

Query Match 3.3%; Score 18; DB 6; Length 595;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
|||||
Db 289 YFLATNYWILVEGLYLH 306

RESULT 12

Q8NHB4 Q8NHB4 PRELIMINARY; PRT; 964 AA.
AC Q8NHB4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,
RA Tetsumi S., Aburatani H., Asai K., Akiyama Y.;
RA "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB06462; BAC05721.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 3.
DR Pfam; PF02793; HRM; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 964 AA; 105706 MW; 8EA72B44244DFD5D CRC64;

Query Match 3.3%; Score 18; DB 4; Length 964;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
|||||
Db 564 YFLATNYWILVEGLYLH 581

RESULT 13

Q8AXV3 Q8AXV3 PRELIMINARY; PRT; 419 AA.
AC Q8AXV3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vasoactive intestinal peptide receptor 1 A.
GN VIPR1A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetradontoidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Cardoso J.C.R., Power D.M., Canario A.V.M., Elgar G., Clark M.S.;
RT "Isolation and characterisation of the VIPR/PACAP receptor gene family
RT in Fugu rubripes";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296144; CAC82588.1; -.
KW Receptor.
SQ SEQUENCE 419 AA; 47607 MW; F21C006AA4E1B698 CRC64;

Query Match 3.0%; Score 16; DB 13; Length 419;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNYIHMLFVSF 187
|||||
Db 130 LHCTRNYIHMLFVSF 145

RESULT 14

Q9IBG2 Q9IBG2 PRELIMINARY; PRT; 418 AA.
AC Q9IBG2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Vasoactive intestinal peptide receptor (Fragment).
GN CVIPR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21218647; PubMed=11319166;
RA Kansaku N., Shimada K., Ohkubo T., Saito N., Suzuki T., Matsuda Y.,
RA Zadworny D.;
RT "Molecular cloning of chicken vasoactive intestinal polypeptide
RT receptor complementary DNA, tissue distribution and chromosomal
RT localization";
RL Biol. Reprod. 64:1575-1581(2001).
DR EMBL; AB029895; BAA95164.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
FT NON TER
SQ SEQUENCE 418 AA; 48191 MW; 7AE4796ADC808FF3 CRC64;

Query Match 2.4%; Score 13; DB 13; Length 418;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNYIHMLF 184
|||||
Db 130 LHCTRNYIHMLF 142

RESULT 15

Q9YHC6 Q9YHC6 PRELIMINARY; PRT; 444 AA.
ID Q9YHC6
AC Q9YHC6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)

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DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Vasoactive intestinal peptide/pituitary adenylate cyclase activating
DE polypeptide receptor.
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=99165178; PubMed=10067855;
RA Alexandre D., Anouar Y., Jegou S., Fournier A., Vaudry H.;
RT "A cloned frog vasoactive intestinal polypeptide/pituitary adenylate
RT cyclase-activating polypeptide receptor exhibits pharmacological and
RT tissue distribution characteristics of both VPAC1 and VPAC2 receptors
RT in mammals."; 140:1285-1293 (1999).
RL Endocrinology
EMBL; AF100644; AAD03602.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Horm; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS02261; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS02261; G_PROTEIN_RECEP_F2_4; 1.
SQ SEQUENCE 444 AA; 50955 MW; 8835259729314C4C CRC64;

Query Match 2.4%; Score 13; DB 13; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNTHMLF 184
DB 157 LHCTRNTHMLF 169

RESULT 16
Q9J140 PRELIMINARY; PRT; 459 AA.
AC Q9J140;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Vasoactive intestinal peptide receptor type 1 (Vasoactive intestinal
DE peptide receptor 1).
GN VIPR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EV6/N;
RA Karacay B., O'Dorisio M.S., Kasow K., Krahe R.;
RT "Cloning and fine Mapping of the Vasoactive Intestinal Peptide
RT Receptor 1 (VPAC1): A Comparative Analysis of Human, Rat and Murine
RT genes.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AF266282; AAF77053.1; -.
DR EMBL; AK052465; BAC35004.1; -.

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DR MGD; MGI:109272; Vipr1.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Horm; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS02261; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS02261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 459 AA; 52095 MW; 9D1ADF8567D4D7F CRC64;

Query Match 2.4%; Score 13; DB 11; Length 459;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNTHMLF 184
DB 171 LHCTRNTHMLF 183

RESULT 17
Q9PVD2 PRELIMINARY; PRT; 542 AA.
AC Q9PVD2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Parathyroid hormone-related protein receptor PTH3R.
GN PTHR3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99428481; PubMed=10497171;
RA Rubin D.A., Juppner H.;
RT "Zebrafish express the common parathyroid hormone/parathyroid hormone-
RT related peptide receptor (PTHrP) and a novel receptor (PTH3R) that is
RT preferentially activated by mammalian and fugu fish parathyroid
RT hormone-related peptide.";
RL J. Biol. Chem. 274:28185-28190 (1999).
DR EMBL; AF132085; AAF01266.2; -.
DR ZFIN; ZDB-GENE-991123-12; pthr3.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Horm; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS02261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 542 AA; 61439 MW; 0868658E2727303 CRC64;

Query Match 2.0%; Score 11; DB 13; Length 542;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 YWILVEGLYLH 262
DB 236 YWILVEGLYLH 246

RESULT 18
Q9J1Y4 PRELIMINARY; PRT; 48 AA.
ID Q9J1Y4

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AC Q9JIV4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE Glucagon-like peptide 2 receptor (Fragment).
 GN GLP2R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SWR/J; TISSUE=Small intestine;
 RA Bierknes M.; Cheng H.;
 RT "Clonal analysis of the effects of glucagon-like peptide 2 (GLP-2) and
 RT keratinocyte growth factor (KGF) on mouse intestinal epithelial
 RT progenitors."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF166265; AAF89584.1; -.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 KW Receptor.
 FT NON_TER 1 48
 FT NON_TER 48
 SQ SEQUENCE 48 AA; 5811 MW; 5D5B18AAEE3AF4AF CRC64;
 Query Match 1.8%; Score 10; DB 11; Length 48;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 172 LHCTRNVIHM 181
 Db |||||
 8 LHCTRNVIHM 17
 RESULT 19
 Q9YHC8 PRELIMINARY; PRT; 167 AA.
 AC Q9YHC8;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DE Glucagon receptor (Fragment).
 OS Rana ridibunda (laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=99165178; PubMed=10067855;
 RA Alexandre D.; Ancuar Y.; Jegou S.; Fournier A.; Vaudry H.;
 RT "A cloned frog vasoactive intestinal polypeptide/pituitary adenylate
 RT cyclase-activating polypeptide receptor exhibits pharmacological and
 RT tissue distribution characteristics of both VPAC1 and VPAC2 receptors
 RT in mammals."
 RL Endocrinology 140:1285-1293(1999).
 DR EMBL; AF100642; AAD03600.1; -.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 FT NON_TER 1 167
 FT NON_TER 167
 SQ SEQUENCE 167 AA; 19505 MW; 07AF68131034F517 CRC64;
 Query Match 1.8%; Score 10; DB 13; Length 167;
 Best Local Similarity 100.0%; Pred. No. 0.095;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 255 LVEGLYLHNL 264

Db |||||
 3 LVEGLYLHNL 12
 RESULT 20
 Q8WUR8 PRELIMINARY; PRT; 227 AA.
 ID Q8WUR8;
 AC Q8WUR8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Hypothetical protein (Fragment).
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervix;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019818; AAH19818.1; -.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 KW Hypothetical protein.
 FT NON_TER 1 1
 FT NON_TER 1
 SQ SEQUENCE 227 AA; 26334 MW; 2D24AEB3EABEC9E5 CRC64;
 Query Match 1.8%; Score 10; DB 4; Length 227;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 172 LHCTRNVIHM 181
 Db |||||
 58 LHCTRNVIHM 67
 RESULT 21
 Q98TU4 PRELIMINARY; PRT; 91 AA.
 ID Q98TU4;
 AC Q98TU4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE Pituitary adenylate cyclase-activating peptide (Fragment).
 GN PACAP.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Wang Y.; Ge W.;
 RT "Cloning of zebrafish ovarian pituitary adenylate cyclase-activating
 RT peptide (PACAP) and regulation of its expression in the ovary."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF329633; AAK08503.1; -.
 DR ZFIN; ZDB-GENE-010406-4; pacap.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 FT NON_TER 1 91
 FT NON_TER 91
 SQ SEQUENCE 91 AA; 10240 MW; 8C9F532D8AD29BC CRC64;
 Query Match 1.7%; Score 9; DB 13; Length 91;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ296143; CAC82587.1; -.

KW Receptor.

SQ SEQUENCE 419 AA; 47662 MW; 0B7A764B53BA2A7E CRC64;

Query Match 1.7%; Score 9; DB 13; Length 419;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIH 180

Db 133 LHCTRNVIH 141

RESULT 26

Q8BGA4

ID Q8BGA4 PRELIMINARY; PRT; 459 AA.

AC Q8BGA4;

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Pituitary adenylate cyclase activating polypeptide type I receptor

DE precursor (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs."

RL Nature 420:563-573(2002).

DR EMBL; AK047304; BAC33020.1; -.

DR EMBL; AK081121; BAC38140.1; -.

FT NON TER 1

SQ SEQUENCE 459 AA; 52407 MW; B0B49556988E96DA CRC64;

Query Match 1.7%; Score 9; DB 11; Length 459;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSFMLRA 191

Db 183 LFVSFMLRA 191

RESULT 27

O73769

ID O73769 PRELIMINARY; PRT; 465 AA.

AC O73769;

DT 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Pituitary adenylate cyclase activating polypeptide type 1

DE receptor.

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Carassius.

OX NCBI_TaxID=7957;

RN [1]

RP SEQUENCE FROM N.A.

RA Wong A.O.L., Leung M.Y., Shea W.L.C., Chang J.P., Chow B.K.C.;

RT "Hypophysiotropic action of pituitary adenylate cyclase activating

RT polypeptide (PACAP) in the goldfish: immunohistochemical demonstration

RT of PACAP in the pituitary, PACAP stimulation of growth hormone release

RT from pituitary cells, and molecular cloning of pituitary type 1 PACAP

RT receptor."

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF048820; AAC15699.1; -.

DR InterPro; IPR000832; GPCR_secretin.

DR InterPro; IPR001879; hormn_receptor.

DR Pfam; PF00002; 7tm_2; 1.

DR Pfam; PF02793; HRM; 1.

DR PRINTS; PR00249; GPCRSECRETIN.

DR SMART; SM00008; Hormr; 1.

DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.

DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.

DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.

DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.

KW Receptor.

SQ SEQUENCE 465 AA; 53459 MW; 9779A95EDBFD1DC1 CRC64;

Query Match 1.7%; Score 9; DB 13; Length 465;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSFMLRA 191

Db 184 LFVSFMLRA 192

RESULT 28

Q8K0B5

ID Q8K0B5 PRELIMINARY; PRT; 485 AA.

AC Q8K0B5;

DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Glucagon receptor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Strausberg R.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC031885; AAH31885.1; -.

DR InterPro; IPR000832; GPCR_secretin.

DR InterPro; IPR001879; hormn_receptor.

DR Pfam; PF00002; 7tm_2; 1.

DR Pfam; PF02793; HRM; 1.

DR PRINTS; PR00249; GPCRSECRETIN.

DR SMART; SM00008; Hormr; 1.

DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.

DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.

DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.

DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.

KW Receptor.

SQ SEQUENCE 485 AA; 54929 MW; 578EB30BF281E67A CRC64;

Query Match 1.7%; Score 9; DB 11; Length 485;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIH 180

Db 170 LHCTRNVIH 178

RESULT 29

Q8BLT3

ID Q8BLT3 PRELIMINARY; PRT; 496 AA.

AC Q8BLT3;

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Pituitary adenylate cyclase activating polypeptide type I receptor

DE precursor.

OS Mus musculus (Mouse).

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DE  Corticotropin releasing hormone receptor variant 1g (Fragment).
GN  CRHR1.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RT  Pisarchik A., Slominski A.T.;
RA  "Alternative splicing of CRH-R1 receptors in human and mouse skin:
RT  identification of new variants and their differential expression.";
RL  FASEB J. 0:0-0(2001).
DR  EMBL; AF369653; AML46633.1; -.
DR  InterPro; IPR000832; GPCR_secretin.
DR  Pfam; PF00002; 7tm_2; 1.
DR  PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR  Receptor.
FT  NON_TER 1 1
FT  NON_TER 37 37
FT  NON_TER 37 37
SQ  SEQUENCE 37 AA; 4488 MW; AE2A8DCD18B35517 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 37;
Best Local Similarity 100.0%; Pred.No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 SFQGFVVS 410
Db 14 SFQGFVVS 21

RESULT 32
OS7671 PRELIMINARY; PRT; 126 AA.
AC OS7671;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Parathyroid hormone receptor (Fragment).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RA Hu C., You S., El Halawani M.E., Foster D.N.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U94326; AAB93893.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR02049; GPCRSECRETIN.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
FT NON_TER 1 1
FT NON_TER 126 126
FT NON_TER 126 AA; 14515 MW; 0F381BDB094A1A77 CRC64;
SQ SEQUENCE 126 AA; 14515 MW; 0F381BDB094A1A77 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 126;
Best Local Similarity 100.0%; Pred.No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYLH 262
Db 6 LVEGLYLH 13

RESULT 33
Q9YHC7 PRELIMINARY; PRT; 168 AA.
ID Q9YHC7
AC Q9YHC7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Secretin receptor (Fragment).

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OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=99165178; PubMed=10067855;
 RA Alexandre D., Anouar Y., Jegou S., Fournier A., Vaudry H.;
 RT "A cloned frog vasoactive intestinal polypeptide/pituitary adenylate
 cyclase-activating polypeptide receptor exhibits pharmacological and
 tissue distribution characteristics of both VPAC1 and VPAC2 receptors
 in mammals.";
 RL Endocrinology 140:1285-1293 (1999).
 DR EMBL; AF100643; AAD03601.1; -;
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm 2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 168
 SQ SEQUENCE 168 AA; 19610 MW; 2EDD1A4B16916FB2 CRC64;
 Query Match 1.5%; Score 8; DB 13; Length 168;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 255 LVEGLYLH 262
 Db |||||
 3 LVEGLYLH 10
 RESULT 34
 Q8BM22 PRELIMINARY; PRT; 304 AA.
 AC Q8BM22;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to glucagon-like peptide 2 receptor precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK035702; BAC29159.1; -;
 SQ SEQUENCE 304 AA; 34448 MW; B668FDA12EB9FD4D CRC64;
 Query Match 1.5%; Score 8; DB 11; Length 304;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 255 LVEGLYLH 262
 Db |||||
 72 LVEGLYLH 79
 RESULT 35
 Q8RM00 PRELIMINARY; PRT; 379 AA.
 AC Q8RM00;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Acyl coenzyme A dehydrogenase.
 GN HCAD.
 OS Acinetobacter sp. ADP1.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=62977;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADP1;
 RX MEDLINE=90130333; PubMed=2298704;
 RA Hartnett C., Neidle E.L., Ngai K.L., Ornston L.N.;
 RT "DNA sequences of genes encoding Acinetobacter calcoaceticus
 protocatechuate 3,4-dioxygenase: evidence indicating shuffling of
 genes and of DNA sequences within genes during their evolutionary
 divergence.";
 RL J. Bacteriol. 172:956-966 (1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADP1;
 RX MEDLINE=93194074; PubMed=8449410;
 RA DiMarco A.A., Averhoff B.A., Kim E.E., Ornston L.N.;
 RT "Evolutionary divergence of poba, the structural gene encoding p-
 hydroxybenzoate hydroxylase in an Acinetobacter calcoaceticus strain
 well-suited for genetic analysis.";
 RL Gene 125:25-33 (1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADP1;
 RX MEDLINE=93323229; PubMed=8331077;
 RA DiMarco A.A., Averhoff B., Ornston L.N.;
 RT "Identification of the transcriptional activator pobr and
 characterization of its role in the expression of poba, the structural
 gene for p-hydroxybenzoate hydroxylase in Acinetobacter
 calcoaceticus.";
 RL J. Bacteriol. 175:4499-4506 (1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADP1;
 RX MEDLINE=94237485; PubMed=8181753;
 RA Hartnett G.B., Ornston L.N.;
 RT "Acquisition of apparent DNA slippage structures during extensive
 evolutionary divergence of pbad and catD genes encoding identical
 catalytic activities in Acinetobacter calcoaceticus.";
 RL Gene 142:23-29 (1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADP1;
 RX MEDLINE=94341565; PubMed=8063101;
 RA Kowalchuk G.A., Hartnett G.B., Benson A., Houghton J.E., Ngai K.L.,
 RA Ornston L.N.;
 RT "Contrasting patterns of evolutionary divergence within the
 Acinetobacter calcoaceticus pca operon.";
 RL Gene 146:23-30 (1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADP1;
 RX MEDLINE=95095936; PubMed=8002591;
 RA Elsemore D.A., Ornston L.N.;
 RT "The pca-pob supraparomic cluster of Acinetobacter calcoaceticus
 contains quia, the structural gene for quinate-shikimate
 dehydrogenase.";
 RL J. Bacteriol. 176:7659-7666 (1994).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADP1;
 RX MEDLINE=98175676; PubMed=9515921;
 RA Gerischer U., Segura A., Ornston L.N.;
 RT "Pcau, a transcriptional activator of genes for protocatechuate
 utilization in Acinetobacter.";
 RL J. Bacteriol. 180:1512-1524 (1998).
 RN [8]
 RP SEQUENCE FROM N.A.


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RC STRAIN=ADP1;
RA Smith M.A., Young D.M., Ornston L.N.;
RT "Genetic analysis of the metabolism of phenylpropanoid compounds in
RL Acinetobacter strain ADP1.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; L05770; AAL54851.1; -.
DR InterPro; IPR006089; Acyl-CoA dh.
DR InterPro; IPR006090; Acyl-CoA dh C.
DR InterPro; IPR006091; Acyl-CoA dh M.
DR InterPro; IPR006092; Acyl-CoA dh N.
DR Pfam; PF00441; Acyl-CoA dh_1.
DR Pfam; PF02770; Acyl-CoA dh_M; 1.
DR Pfam; PF02771; Acyl-CoA dh_N; 1.
DR PROSITE; PS00072; ACYL COA DH 1; 1.
DR PROSITE; PS00073; ACYL COA DH 2; 1.
SQ SEQUENCE 379 AA; 42182 MW; 085705F2EDD70DE3 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 FGSLAVAI 163
Db 79 FGSLAVAI 86
|||||

RESULT 36
Q98UC1 PRELIMINARY; PRT; 405 AA.
AC Q98UC1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Corticotropin releasing factor receptor 2.
OS Aneurus nebulosus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ameiurus.
OX NCBI_TaxID=27778;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066341; PubMed=11145609;
RA Arai M., Assil I.Q., Abou-Samra A.B.;
RT "Characterization of Three Corticotropin-Releasing Factor Receptors in
RT Catfish: A Novel Third Receptor Is Predominantly Expressed in
RT Pituitary and Urophysis.";
RL Endocrinology 142:446-454(2001).
DR EMBL; AF229360; AAK01089.1; -.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 405 AA; 46823 MW; E05E96BCFEAD5CC5 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 405;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
Db 343 SFQGFVVS 350
|||||

RESULT 37
Q8WML9 PRELIMINARY; PRT; 410 AA.
ID Q8WML9
AC Q8WML9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Corticotropin-releasing factor receptor type 2.
GN CSFR2.
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Pohl S., Darlison M.G., Lederis K., Richter D.;
RT "Corticotropin-releasing factor receptors from teleost fish:
RT evolutionary conservation of sequence, functional expression and
RT second messenger coupling.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271758; CAC81754.1; -.
KW Receptor.
SQ SEQUENCE 414 AA; 48329 MW; 11FB2E9E481CCC2 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 414;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Corticotropin releasing factor type 2A receptor.
GN CSF2A.
OS Tupiaia belangeri (Northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RA Dautzenberg F.M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99288234; PubMed=10336722;
RA Palchaudhuri M.R., Hauger R.L., Wille S., Dautzenberg F.M.;
RT "Isolation and pharmacological characterization of two functional
RT splice variants of corticotropin-releasing factor type 2 receptor from
RT the tree shrew (Tupaia belangeri).";
RL J. Neuroendocrinol. 11:419-428(1999).
DR EMBL; AJ422242; CAD19578.1; -.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 410 AA; 47613 MW; 09AB660341A63DDC CRC64;

Query Match 1.5%; Score 8; DB 6; Length 410;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
Db 348 SFQGFVVS 355
|||||

RESULT 38
Q8AWA1 PRELIMINARY; PRT; 414 AA.
ID Q8AWA1
AC Q8AWA1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Corticotropin-releasing factor receptor type 2.
GN CSFR2.
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Pohl S., Darlison M.G., Lederis K., Richter D.;
RT "Corticotropin-releasing factor receptors from teleost fish:
RT evolutionary conservation of sequence, functional expression and
RT second messenger coupling.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271758; CAC81754.1; -.
KW Receptor.
SQ SEQUENCE 414 AA; 48329 MW; 11FB2E9E481CCC2 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 414;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 403 SFQGFVS 410
Db 352 SFQGFVS 359

RESULT 39
Q9BGU4 PRELIMINARY; PRT; 415 AA.
ID Q9BGU4;
AC Q9BGU4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Corticotropin-releasing hormone receptor.
GN CRFR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Holstein;
RA Takata M., Sekikawa K.;
RT "Molecular Cloning of Bovine corticotropin-releasing hormone receptor
RT cDNA.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB055434; BAB21864.1; -.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
XW Receptor.
SQ SEQUENCE 415 AA; 47754 MW; 4A54A3DCE6CF2319 CRC64;

Query Match 1.5%; Score 8; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVS 410
Db 353 SFQGFVS 360

RESULT 40
Q8WMM0 PRELIMINARY; PRT; 415 AA.
ID Q8WMM0;
AC Q8WMM0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Corticotropin releasing factor type 1 receptor.
GN CRF1.
OS Tupia belangeri (Northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiidae.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC Dautzenberg F.M.;
RA Dautzenberg F.M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99067019; PubMed=9851694;
RA Palchaudhuri M.R., Wille S., Mevenkamp G., Spiess J., Fuchs E.,
RA Dautzenberg F.M.;
RT "Corticotropin-releasing factor receptor type 1 from Tupia belangeri:
RT cloning, functional expression and tissue distribution.";
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RL Eur. J. Biochem. 258:78-84(1998).
DR EMBL; AJ422241; CAD19577.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
XW Receptor.
SQ SEQUENCE 415 AA; 47685 MW; 97BE9AEB050AC08D CRC64;

Query Match 1.5%; Score 8; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVS 410
Db 353 SFQGFVS 360

RESULT 41
Q8K3R2 PRELIMINARY; PRT; 415 AA.
ID Q8K3R2;
AC Q8K3R2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type-1 corticotropin-releasing hormone receptor alpha isoform.
GN CRH-R1.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Pisarchik A.V., Slominski A.;
RT "Hamster CRH receptor type 1 (alpha) mRNA coding sequence.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034599; AAK59707.1; -.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
XW Receptor.
SQ SEQUENCE 415 AA; 47703 MW; 500B4DD617E5F19E CRC64;

Query Match 1.5%; Score 8; DB 11; Length 415;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVS 410
Db 353 SFQGFVS 360

RESULT 42
Q98UC0 PRELIMINARY; PRT; 428 AA.
ID Q98UC0;
AC Q98UC0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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DE OS Corticotropin releasing factor receptor 3.
OC Ameiurus nebulosus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ameiurus.
OX NCBI_TaxID=27778;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066341; PubMed=11145609;
RA Arai M., Assil I.Q., Abou-Samra A.B.;
RT "Characterization of Three Corticotropin-Releasing Factor Receptors in
RT Catfish: A Novel Third Receptor Is Predominantly Expressed in
RT Pituitary and Urophysis.";
RL Endocrinology 142:446-454(2001).
DR EMBL; AF229361; AAK01070.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; HORMR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 428 AA; 49406 MW; 63F9C07AFFEF5B27 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 428;
Best Local Similarity 100.0%; Pred.No.29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 SFQGFVVS 410
Db 366 SFQGFVVS 373

RESULT 43
Q8AWA2 PRELIMINARY; PRT; 430 AA.
AC Q8AWA2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Corticotropin-releasing factor receptor type 1.
GN CRFRL.
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Pohl S., Darlison M.G., Lederis K., Richter D.;
RT "Corticotropin-releasing factor receptors from teleost fish:
RT evolutionary conservation of sequence, functional expression and
RT second messenger coupling.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ27157; CAC81753.1; -.
KW Receptor.
SQ SEQUENCE 430 AA; 49595 MW; BCD2CDF36B1281A2 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 430;
Best Local Similarity 100.0%; Pred.No.29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 SFQGFVVS 410
Db 368 SFQGFVVS 375

RESULT 44

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Q8WML8 PRELIMINARY; PRT; 437 AA.
ID Q8WML8;
AC Q8WML8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Corticotropin releasing factor type 2B receptor.
GN CRF2B.
OS Tupia belangeri (Northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RX Dautzenberg F.M.;
RA Dautzenberg F.M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99286234; PubMed=10336722;
RA Palchaudhuri M.R., Hauger R.L., Wille S., Fuchs E., Dautzenberg F.M.;
RT "Isolation and pharmacological characterization of two functional
RT splice variants of corticotropin-releasing factor type 2 receptor from
RT the tree shrew (Tupaia belangeri).";
RL J. Neuroendocrinol. 11:419-428(1999).
DR EMBL; AJ422443; CAD19579.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; HORMR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 437 AA; 50330 MW; E471B7D880E1B07 CRC64;

Query Match 1.5%; Score 8; DB 6; Length 437;
Best Local Similarity 100.0%; Pred.No.29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 SFQGFVVS 410
Db 375 SFQGFVVS 382

RESULT 45
Q73768 PRELIMINARY; PRT; 438 AA.
ID Q73768;
AC Q73768;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Growth-hormone releasing hormone-like peptide receptor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX Chan K.W., Yu K.L., Rivier J., Chow B.K.C.;
RA "Identification and characterization of a receptor from goldfish
RT specific for a teleost growth hormone-releasing hormone-like
RT peptide.";
RL Neuroendocrinology 0:0-0(1998).
DR EMBL; AF048819; AAC15698.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.

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DR SMART; SM00008; HORM; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS02227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 438 AA; 50305 MW; C3516A52D692C339 CRC64;
 Query Match 1.5%; Score 8; DB 13; Length 438;
 Best Local Similarity 100.0%; Pred.No.29; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 173 HCTRYN180
 Db 165 HCTRYN172
 RESULT 46
 Q98UC2 PRELIMINARY; PRT; 445 AA.
 AC Q98UC2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Corticotropin releasing factor receptor 1.
 OS Ameiurus nebulosus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ameiurus.
 OC NCBI_TaxID=27778;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21066341; PubMed=11145609;
 RA Arai M., Assil I.Q., Abou-Samra A.B.;
 RT "Characterization of Three Corticotropin-Releasing Factor Receptors in
 RT Catfish: A Novel Third Receptor Is Predominantly Expressed in
 RT Pituitary and Urophysis";
 RL Endocrinology 142:446-454(2001).
 DR EMBL; AF229359; AAK01068.1; -;
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormu_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HORM; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 445 AA; 51062 MW; F17DA70BE22BB755 CRC64;
 Query Match 1.5%; Score 8; DB 13; Length 445;
 Best Local Similarity 100.0%; Pred.No.30; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 403 SFOGFFVS 410
 Db 383 SFOGFFVS 390
 RESULT 47
 Q8NG71 PRELIMINARY; PRT; 447 AA.
 AC Q8NG71;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Seven transmembrane helix receptor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Itutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB065967; BAC06179.1; -;
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormu_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HORM; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 447 AA; 51070 MW; 6C4EDBDC5197FBCD CRC64;
 Query Match 1.5%; Score 8; DB 4; Length 447;
 Best Local Similarity 100.0%; Pred.No.30; Mismatches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 403 SFOGFFVS 410
 Db 385 SFOGFFVS 392
 RESULT 48
 Q8UVY4 PRELIMINARY; PRT; 489 AA.
 AC Q8UVY4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Glucagon receptor.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OC NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21148137; PubMed=11350547;
 RA Sivarajah P., Wheeler M.B., Irwin D.M.;
 RT "Evolution of receptors for proglucagon-derived peptides: isolation of
 RT frog glucagon receptors";
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 128:517-527(2001).
 DR EMBL; AF318179; AAL37167.1; -;
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormu_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETINE; 1.
 KW Receptor.
 SQ SEQUENCE 489 AA; 56746 MW; 39385ECT76D68C84F CRC64;
 Query Match 1.5%; Score 8; DB 13; Length 489;
 Best Local Similarity 100.0%; Pred.No.32; Mismatches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 146 VMYTVGYS 153
 Db 137 VMYTVGYS 144

RESULT 49

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Q8SZ04
ID Q8SZ04 PRELIMINARY; PRT; 580 AA.
AC Q8SZ04;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE RE25570P
GN HEP OR CG2190 OR CG4353. (Fruit fly).
OS Drosophila melanogaster
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY071210; AAL48832.1; -.
DR FlyBase; FBgn0010303; hep.
SQ SEQUENCE 580 AA; 61880 MW; 3596898A7A7A5F9F CRC64;
Query Match 1.5%; Score 8; DB 5; Length 580;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 456 THSTSSQS 463
DB 239 THSTSSQS 246
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RESULT 50
Q917S3
ID Q917S3 PRELIMINARY; PRT; 580 AA.
AC Q917S3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CG4353 protein.
GN HEP OR CG2190 OR CG4353.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Bouchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Markulov G., Milshina N.V., Mobarty C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnick S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003491; AAG22351.2; -.
DR FlyBase; FBgn0010303; hep.
SQ SEQUENCE 580 AA; 61938 MW; 9A96898AB57A5F9E CRC64;
Query Match 1.5%; Score 8; DB 5; Length 580;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 456 THSTSSQS 463
DB 239 THSTSSQS 246
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Search completed: December 9, 2003, 09:02:06
Job time: 42 secs

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OM protein - protein search, using sw model

Run on: November 21, 2003, 22:32:16 ; Search time 21 Seconds
(without alignments)
2477.488 Million cell updates/sec

Title: US-09-996-569-2
Perfect score: 541
Sequence: 1 MAWLGLSLHVMGLMLGSL.....DDILMEKSPRMESNPDTGEG 541

Scoring table: OLIGO
Gap 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1979

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	363	67.1	550	2 A57519	parathyroid hormon
2	25	4.6	585	2 A39286	parathyroid hormon
3	19	3.5	440	2 JC2532	secretin receptor
4	19	3.5	449	2 S16319	secretin receptor
5	18	3.3	589	2 I59297	parathyroid hormon
6	18	3.3	591	2 S44203	parathyroid hormon
7	18	3.3	593	2 A49191	parathyroid hormon
8	18	3.3	593	2 A49191	parathyroid hormon
9	13	2.4	455	2 I53273	gastric inhibitory
10	13	2.4	459	2 JH0594	vasoactive intesti
11	13	2.4	460	2 JC2194	vasoactive intesti
12	13	2.4	462	2 JC2462	gastric inhibitory
13	13	2.4	495	2 JC2195	vasoactive intesti
14	12	2.2	466	2 G02234	gastric inhibitory
15	12	2.2	466	2 S66676	glucose-dependent
16	12	2.2	491	2 I37411	glucose-dependent
17	10	1.8	477	2 JC2041	glucagon receptor
18	9	1.7	381	2 S33449	pituitary adenylat
19	9	1.7	437	2 JU0185	PACAP/VIP receptor
20	9	1.7	437	2 S39069	vasoactive intesti
21	9	1.7	438	2 G02822	vasoactive intesti
22	9	1.7	463	2 S71624	glucagon-like pept
23	9	1.7	463	2 A46172	glucagon-like pept
24	9	1.7	463	2 I84494	glucagon-like pept
25	9	1.7	467	2 JN0616	pituitary adenylat
26	9	1.7	485	2 JQ1957	pituitary adenylat
27	9	1.7	485	2 JC4363	glucagon receptor
28	9	1.7	495	2 S36114	pituitary adenylat
29	9	1.7	495	2 S39061	pituitary adenylat

30	9	1.7	513	2 S47631	pituitary adenylat
31	9	1.7	523	2 S39060	pituitary adenylat
32	9	1.7	525	2 JN0902	pituitary adenylat
33	8	1.5	375	2 I38879	corticotropin rele
34	8	1.5	411	2 A55610	corticotropin-rele
35	8	1.5	411	2 S26195	probable carboxyl-
36	8	1.5	415	2 S39535	corticotropin-rele
37	8	1.5	415	2 I58144	corticotropin-rele
38	8	1.5	430	2 A56726	corticoliberin rec
39	8	1.5	431	2 I49279	sauvagine/corticot
40	8	1.5	431	2 I49149	CRF receptor - mou
41	8	1.5	444	2 A48260	corticoliberin rec
42	8	1.5	533	1 GRBYCP	cytosine/purine tr
43	8	1.5	1304	2 T13256	tail-host specific
44	7	1.3	50	2 B37334	L-mandelate dehydr
45	7	1.3	80	2 AB2755	host factor I [imp

ALIGNMENTS

RESULT 1

A57519
parathyroid hormone receptor 2 precursor - human
N:Alternate names: PTH2 receptor
C:Species: ~~Human~~ - ~~Humans~~ (man)
C>Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999
C:Accession: A57519
R:Usdin, T.B.; Gruber, C.; Bonner, T.I.
J. Biol. Chem. 270, 15455-15458, 1995
A:Title: Identification and functional expression of a receptor selectively recognizing
A:Reference number: A57519; MUID:95318121; PMID:7797535
A:Accession: A57519
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-550 <USD>
A:Cross-references: GB:U25128; NID:9887966; PIDN:AAC50157.1; PID:9887967
C:Genetics:
A:Gene: GDB: PTHR2; PTHR2R
A:Cross-references: GDB:731977; OMIM:601469
A:Map position: 2q33-2q33
C:Superfamily: glucagon receptor
C:Keywords: hormone receptor

Query Match	67.1%;	Score 363;	DB 2;	Length 550;	
Best Local Similarity	99.8%;	Pred. No. 0;			
Matches 463;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	4	LGASLHVWGLMLGSCLLAR	QQLDSGGTTTIEEQIVLVKAKVQCELNITAQLOQEGGNC	63	
Db	4	LGASLHVWGLMLGSCLLAR	QQLDSGGTTTIEEQIVLVKAKVQCELNITAQLOQEGGNC	63	
QY	64	FPEWDGLICWPRGTGKISAV	CCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWANY	123	
Db	64	FPEWDGLICWPRGTGKISAV	CCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWANY	123	
QY	124	DCLEFLQPDISIGKQEFCE	RLRYVMYTVGYSISFSGSLAVAILIIGYFRRLHCTRN	183	
Db	124	DCLEFLQPDISIGKQEFCE	RLRYVMYTVGYSISFSGSLAVAILIIGYFRRLHCTRN	183	
QY	184	FVSPMLRATSFVKDRVV	HAHIGVKELESIMQDDPONSIEATSDVKSOYIGCKIAVMVF	243	
Db	184	FVSPMLRATSFVKDRVV	HAHIGVKELESIMQDDPONSIEATSDVKSOYIGCKIAVMVF	243	
QY	244	IYFLATNYWTLVBGLYH	NLIIFVAFSDTKYLMGFFILIGWGFPAFVA	303	
Db	244	IYFLATNYWTLVBGLYH	NLIIFVAFSDTKYLMGFFILIGWGFPAFVA	303	
QY	304	ARCWELSGADIKWIYQ	APILAAIGLNFILFLNTRVRLATKIWETNAVGHDTKQYRKLAK	363	
Db	304	ARCWELSGADIKWIYQ	APILAAIGLNFILFLNTRVRLATKIWETNAVGHDTKQYRKLAK	363	
QY	364	STLVLVLVFGVHYIVF	VCLPHSFTGLGWIEIRMHCELFNFSFGFFVSIITYCNCGEVQAE	423	

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Db 364 STLVLVLVFGVHYIIVFCLPHSFTGLGWEIRHCELFNSFGQFVFSIYYCYCNGEVOAE 423
QY 424 VKQWMSRWNLSDVWKRTPPCGSRRCGSVLTVTWTHSTSSQSQA 467
Db 424 VKQWMSRWNLSDVWKRTPPCGSRRCGSVLTVTWTHSTSSQSQA 467

RESULT 2
A39286
parathyroid hormone / parathyroid hormone-related peptide - North American opossum
C:Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 11-Jan-2000
C:Accession: A39286
R:Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; K
Science 254, 1024-1026, 1991
A:Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-rel
A:Reference number: A39286; MUID:92054592; PMID:1658941
A:Accession: A39286
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-585 <JUE>
A:Cross-references: GB:M74445
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 6.5e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNYYIHMLFVSPMLRA 191
Db 207 GYFRLHCTRNYYIHMLFVSPMLRA 231

RESULT 3
JC2532
secretin receptor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
C:Accession: JC2532
R:Jiang, S.; Ulrich, C.
Biochem. Biophys. Res. Commun. 207, 883-890, 1995
A:Title: Molecular cloning and functional expression of a human pancreatic secretin rece
A:Reference number: JC2532; MUID:95169147; PMID:7864894
A:Accession: JC2532
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-440 <JIA>
A:Cross-references: EMBL:U20178; NID:G662795; PIDN:AAC50106.1; PID:G662796
A:Experimental source: pancreas
C:Genetics:
A:Gene: GDB:SCTR
A:Cross-references: GDB:270546; ONTM:182098
A:Map position: 2q14.1-2q14.1
C:Superfamily: glucagon receptor

Query Match 3.5%; Score 19; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYYIHMLFVSP 187
Db 167 FRLHCTRNYYIHMLFVSP 185

RESULT 4
S16319
secretin receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S16319
R:Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.
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EMBO J. 10, 1635-1641, 1991
A:Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
A:Reference number: S16319; MUID:91266890; PMID:1646711
A:Accession: S16319
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-449 <ISH>
A:Cross-references: EMBL:X59132; NID:G57228; PIDN:CAA41849.1; PID:G57229
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.5%; Score 19; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 7.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYYIHMLFVSP 187
Db 167 FRLHCTRNYYIHMLFVSP 185

RESULT 5
159297
parathyroid hormone/parathyroid hormone related-peptide receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: 159297
R:McCuagig, K.A.; Clarke, J.C.; White, J.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994
A:Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parathyr
A:Reference number: 159297; MUID:94255468; PMID:8197183
A:Accession: 159297
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-589 <RES>
A:Cross-references: GB:L34611; NID:G530149; PIDN:AAA40011.1; PID:G530151
C:Genetics:
A:Gene: PTHR
A:Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2;
C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYWILVEGLYLH 262
Db 290 YFLATNYYWILVEGLYLH 307

RESULT 6
S44203
parathyroid hormone-related peptide receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C:Accession: S44203
R:Karperien, M.; van Dijk, T.B.; Hoeijmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boons
submitted to the EMBL Data Library, April 1994
A:Description: Expression pattern of parathyroid hormone/parathyroid hormone related p
A:Reference number: S44203
A:Accession: S44203
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-591 <KAR>
A:Cross-references: EMBL:X78936; NID:G474828; PIDN:CAA55536.1; PID:G474829
C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 9.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYWILVEGLYLH 262
Db 290 YFLATNYYWILVEGLYLH 307
```

RESULT 7
154195

parathyroid hormone/parathyroid hormone related-peptide receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jan-2000
 C:Accession: I54195; A42698
 R:Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier
 Genomics 20, 20-26, 1994
 A>Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor
 and rat genomes.

A:Reference number: I54195; MUID:94292182; PMID:8020952

A:Accession: I54195

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-591 <RES>

A:Cross-references: GB:L19475; NID:g467316; PIDN:AAAG8098.1; PID:g467317
 R:Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure
 Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992

A>Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid
 n of both cAMP and inositol triphosphates and increases intracellular free calcium.

A:Reference number: A42698; MUID:92212903; PMID:1313566

A:Accession: A42698

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-585,'G',587-591 <ABO>

A:Experimental source: ROS 17/2.8 osteosarcoma cells

A>Note: sequence extracted from NCBI backbone (NCBIP:92187)

C:Superfamily: glucagon receptor

Query Match

Best Local Similarity 3.3%; Score 18; DB 2; Length 591;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYH 262

|||||

Db 290 YFLATNYWILVEGLYH 307

RESULT 8

A49191

parathyroid hormone/PTH-related peptide receptor - human
 N:Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor
 C:Species: Homo sapiens (man)

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000

C:Accession: I38139; A49191; I38113; G01562; S29610

R:Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhmann, M.
 Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Juppner, H.
 J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995

A>Title: Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons

A:Reference number: I38139; MUID:95263723; PMID:7745008

A:Accession: I38139

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-593 <RES>

A:Cross-references: EMBL:U22409; NID:g897594; PIDN:AAAG0657.1; PID:g897596

R:Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V.
 Endocrinology 132, 2157-2165, 1993

A>Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pe

A:Reference number: A49191; MUID:93238641; PMID:8386612

A:Accession: A49191

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-593 <SCH>

A:Cross-references: GB:L04308; NID:g190721; PIDN:AAA36525.1; PID:g190722

A>Note: sequence extracted from NCBI backbone (NCBIN:130233, NCBIP:130234)
 R:Schneider, H.; Feyen, J.H.; Seuwen, K.; Morva, N.R.
 Eur. J. Pharmacol. 246, 149-155, 1993

A>Title: Cloning and functional expression of a human parathyroid hormone receptor.

A:Reference number: I38113; MUID:93387403; PMID:8397094

A:Accession: I38113

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-593 <RE2>

A:Cross-references: EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PID:g396813

R:Levine, M.

submitted to the EMBL Data Library, November 1994

A:Reference number: G07787

A:Accession: G01562

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-593 <LEV>

A:Cross-references: EMBL:U17418; NID:g596129; PIDN:AAA56774.1; PID:g596130

C:Genetics:

A:Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2;

C:Superfamily: glucagon receptor

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 3.3%; Score 18; DB 2; Length 593;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYH 262

|||||

Db 290 YFLATNYWILVEGLYH 307

RESULT 9

153273

gastric inhibitory polypeptide receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Sep-1999

C:Accession: I53273

R:Usdin, T.B.; Mezey, E.; Button, D.C.; Brownstein, M.J.; Bonner, T.I.

Endocrinology 133, 2861-2870, 1993

A>Title: Gastric inhibitory polypeptide receptor, a member of the secretin-vasoactive

A:Reference number: I53273; MUID:94062667; PMID:8243312

A:Accession: I53273

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-455 <RES>

A:Cross-references: GB:L19660; NID:g431448; PIDN:AAAC37637.1; PID:g431449

C:Superfamily: glucagon receptor

Query Match

Best Local Similarity 2.4%; Score 13; DB 2; Length 455;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRRLHCTRNVIHM 181

|||||

Db 159 FRRLHCTRNVIHM 171

RESULT 10

JH0594

vasoactive intestinal peptide receptor precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C:Accession: JH0594; S56014

R:Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.

Neuron 8, 811-819, 1992

A>Title: Functional expression and tissue distribution of a novel receptor for vasoact

A:Reference number: JH0594; MUID:92232309; PMID:1314625

A:Accession: JH0594

A:Molecule type: mRNA

A:Residues: 1-459 <ISH>

A:Cross-references: GB:M86835; NID:g207640; PIDN:AAA42331.1; PID:g207641

A:Experimental source: lung

R:Pei, L.; Melmed, S.

Biochem. J. 308, 719-723, 1995

A>Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene 5

A:Reference number: S56014; MUID:97104266; PMID:8948424

A:Accession: S56014

A>Status: preliminary; translation not shown

A:Molecule type: DNA

A;Residues: 1-26 <PEI>
A;Cross-references: EMBL:U10635; NID:g505752; PIDN:AAB48185.1; PID:g514311
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>
F;146-166/Domain: transmembrane #status predicted <TM1>
F;176-195/Domain: transmembrane #status predicted <TM2>
F;218-241/Domain: transmembrane #status predicted <TM3>
F;256-277/Domain: transmembrane #status predicted <TM4>
F;295-318/Domain: transmembrane #status predicted <TM5>
F;344-363/Domain: transmembrane #status predicted <TM6>
F;376-395/Domain: transmembrane #status predicted <TM7>
F;58,69,100,292/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
|||||
Db 171 LHCTRNVIHMLF 183
|||||

RESULT 11
JC2194
vasoactive intestinal peptide receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 07-Oct-1994 #text_change 05-Nov-1999
C;Accession: JC2194; JN0604; EC2289; S38397
R;Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Denis
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A;Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA en
A;Reference number: JC2194; MUID:94235025; PMID:8179610
A;Accession: JC2194
A;Molecule type: mRNA
A;Residues: 1-460 <CO>
A;Cross-references: EMBL:X75299; NID:g407461; PIDN:CAAS3046.1; PID:g407462
A;Experimental source: jejunal epithelial cell; clone hIVR8
R;Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.
Biochem. Biophys. Res. Commun. 193, 546-553, 1993
A;Title: Cloning and functional expression of a human neuroendocrine vasoactive intestin
A;Reference number: JN0604; MUID:93290841; PMID:8390245
A;Accession: JN0604
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-284,288-460 <SRE>
A;Cross-references: GB:L13288; NID:g292903; PIDN:AAA36805.1; PID:g292904
R;Couvineau, A.; Gaudin, P.; Maoret, J.J.; Rouyer-Fessard, C.; Nicole, P.; Laburthe, M.
Biochem. Biophys. Res. Commun. 206, 246-252, 1995
A;Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-terminal
A;Reference number: PC2289; MUID:95118345; PMID:7818527
A;Accession: PC2289
A;Molecule type: mRNA
A;Residues: 63-129 <CO2>
C;Genetics:
A;Gene: GDB:VIPR1; RCD1; HVRI
A;Cross-references: GDB:128589; OMIM:192321
A;Map position: 3p22-3p22
C;Superfamily: glucagon receptor
C;Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane pro
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-460/Product: vasoactive intestinal peptide receptor #status predicted <MAT>
F;146-166/Domain: transmembrane #status predicted <TM1>
F;176-194/Domain: transmembrane #status predicted <TM2>
F;216-234/Domain: transmembrane #status predicted <TM3>
F;255-277/Domain: transmembrane #status predicted <TM4>
F;299-319/Domain: transmembrane #status predicted <TM5>
F;346-363/Domain: transmembrane #status predicted <TM6>
F;377-396/Domain: transmembrane #status predicted <TM7>
F;58,69,100,293/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;76/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F;250/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

F;450/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
|||||
Db 170 LHCTRNVIHMLF 182
|||||

RESULT 12
JC2462
gastric inhibitory polypeptide receptor - hamster
N;Alternate names: GIP receptor
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2462
R;Yasuda, K.; Inagaki, N.; Yamada, Y.; Kubota, A.; Seino, S.; Seino, Y.
Biochem. Biophys. Res. Commun. 205, 1556-1562, 1994
A;Title: Hamster gastric inhibitory polypeptide receptor expressed in pancreatic islet
A;Reference number: JC2462; MUID:95110292; PMID:7811236
A;Accession: JC2462
A;Molecule type: mRNA
A;Residues: 1-462 <YAS>
A;Cross-references: DDBJ:D38103; NID:g644880; PIDN:BAA07284.1; PID:g765087
C;Superfamily: glucagon receptor
C;Keywords: receptor; transmembrane protein
F;136-157/Domain: transmembrane #status predicted <TM1>
F;167-186/Domain: transmembrane #status predicted <TM2>
F;215-238/Domain: transmembrane #status predicted <TM3>
F;252-274/Domain: transmembrane #status predicted <TM4>
F;292-315/Domain: transmembrane #status predicted <TM5>
F;339-357/Domain: transmembrane #status predicted <TM6>
F;383-394/Domain: transmembrane #status predicted <TM7>

Query Match 2.4%; Score 13; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIHM 181
|||||
Db 159 FRLHCTRNVIHM 171
|||||

RESULT 13
JC2195
vasoactive intestinal peptide receptor-related protein precursor (clone hIVR5) - human
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
C;Accession: JC2195; S42087
R;Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Der
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A;Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA
A;Reference number: JC2194; MUID:94235025; PMID:8179610
A;Accession: JC2195
A;Molecule type: mRNA
A;Residues: 1-495 <COU>
A;Cross-references: EMBL:X77777; NID:g456352; PIDN:CAA54814.1; PID:g456353
A;Experimental source: jejunal epithelial cell
C;Genetics:
A;Gene: GDB:VIPR1; RCD1; HVRI
A;Cross-references: GDB:128589; OMIM:192321
A;Map position: 3p22-3p22
C;Superfamily: glucagon receptor
C;Keywords: glycoprotein; intestine; phosphoprotein; receptor; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-495/Product: vasoactive intestinal peptide receptor-related protein #status predi
F;180-203/Domain: transmembrane #status predicted <TM1>
F;211-229/Domain: transmembrane #status predicted <TM2>
F;251-269/Domain: transmembrane #status predicted <TM3>
F;290-312/Domain: transmembrane #status predicted <TM4>
F;334-354/Domain: transmembrane #status predicted <TM5>

Search completed: November 21, 2003, 22:35:55
Job time : 22 secs

F;381-398/Domain: transmembrane #status predicted <TM6>
F;412-431/Domain: transmembrane #status predicted <TM7>
F;93,104,135,328/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;111/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F;285/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F;485/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIHMLF 184
|||
Db 205 LHCTRYIHMLF 217
|||

RESULT 14

G02234
gastric inhibitory polypeptide receptor - human
N;Alternate names: GIP receptor
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
C;Accession: G02234
R;Bonner, T.I.; Usdin, T.B.
submitted to the EMBL Data Library, October 1995
A;Reference number: G09336
A;Accession: G02234
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-466 <BON>
A;Cross-references: EMBL:U39231; NID:g1066050; PIDN:AAA84418.1; PID:g1066051
C;Genetics:
A;Gene: GDB:GIPR
A;Cross-references: GDB:335023
A;Map position: 19q13.3-19q13.3
C;Superfamily: glucagon receptor

Query Match 2.2%; Score 12; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYIH 180
|||
Db 162 FRLHCTRYIH 173
|||

RESULT 15

S66676
glucose-dependent insulinotropic protein receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S66676
R;Volz, A.; Goeke, R.; Lankat-Buttgereit, B.; Fehmann, H.C.; Bode, H.P.; Goeke, B.
FEBS Lett. 373, 23-29, 1995
A;Title: Molecular cloning, functional expression, and signal transduction of the GIP-receptor
A;Reference number: S66676; MUID:96013879; PMID:7589426
A;Accession: S66676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-466 <VOL>
A;Cross-references: GB:S79852
A;Note: the authors translated the codon GCC for residue 427 as Leu
C;Superfamily: glucagon receptor
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-466/Product: glucose-dependent insulinotropic protein receptor #status predicted <M

Query Match 2.2%; Score 12; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYIH 180
|||
Db 162 FRLHCTRYIH 173
|||

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 22:28:35 ; Search time 17 Seconds
(without alignments)
1496.556 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGAHLHYVWGLMGLSCL.....DDLMEKPSRPMESNPDPTEG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 6

Total number of hits satisfying chosen parameters: 905

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	363	67.1	550	1 PTHR2_HUMAN	P49190 homo sapien
2	33	6.1	546	1 PTHR2_RAT	P70555 rattus norv
3	25	4.6	585	1 PTHR2_DIDMA	P25107 didelphis m
4	19	3.5	440	1 SCRC_HUMAN	P47872 homo sapien
5	19	3.5	449	1 SCRC_RAT	P23811 rattus norv
6	18	3.3	585	1 PTHR_PIG	P50133 sus scrofa
7	18	3.3	591	1 PTHR_MOUSE	P41593 mus musculus
8	18	3.3	591	1 PTHR_RAT	P25961 rattus norv
9	18	3.3	593	1 PTHR_HUMAN	Q03431 homo sapien
10	16	3.0	445	1 SCRC_RABIT	O46502 oryctolagus
11	16	3.0	447	1 VIPR_CARAU	Q90308 carassius a
12	13	2.4	455	1 GIPR_RAT	P43219 rattus norv
13	13	2.4	457	1 VIPR_HUMAN	P32241 homo sapien
14	13	2.4	457	1 VIPR_MELGA	Q91085 meleagris g
15	13	2.4	458	1 VIPR_PIG	Q28992 sus scrofa
16	13	2.4	459	1 VIPR_MOUSE	P97751 mus musculus
17	13	2.4	459	1 VIPR_RAT	P30083 rattus norv
18	13	2.4	462	1 GIPR_VESAU	P43218 mesocricetu
19	12	2.2	466	1 GIPR_HUMAN	P48546 homo sapien
20	10	1.8	477	1 GLR_HUMAN	P47871 homo sapien
21	10	1.8	550	1 GLP2_RAT	Q940W0 rattus norv
22	10	1.8	553	1 GLP2_HUMAN	Q95838 homo sapien
23	9	1.7	437	1 VIPR_MOUSE	P41588 mus musculus
24	9	1.7	437	1 VIPR_RAT	P35000 rattus norv
25	9	1.7	438	1 VIPR_HUMAN	P41587 homo sapien
26	9	1.7	463	1 GLPI_HUMAN	P43220 homo sapien
27	9	1.7	463	1 GLPI_RAT	P32301 rattus norv
28	9	1.7	468	1 PACR_HUMAN	P41586 homo sapien
29	9	1.7	485	1 GLR_MOUSE	Q61606 mus musculus
30	9	1.7	485	1 GLR_RAT	P30082 rattus norv
31	9	1.7	489	1 GLPI_MOUSE	Q35659 mus musculus
32	9	1.7	496	1 PACR_MOUSE	P70205 mus musculus
33	9	1.7	513	1 PACR_BOVIN	Q29627 bos taurus

RESULT 1

ID	PTR2_HUMAN	STANDARD;	PRT;	550 AA.
AC	P49190;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Parathyroid hormone receptor precursor (PTH2 receptor).			
GN	PTH2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.			
RC	TISSUE=Brain;			
RX	MEDLINE=95318121; PubMed=7797535;			
RA	Usdin T.B., Gruber C., Bonner T.I.;			
RT	"Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor.";			
RL	J. Biol. Chem. 270:15455-15458(1995).			
RN	[2]			
RP	SEQUENCE OF 26-40 AND 306-550 FROM N.A.			
RX	MEDLINE=97079671; PubMed=8921382;			
RA	Usdin T.B., Modi W., Bonner T.I.;			
RT	"Assignment of the human PTH2 receptor gene (PTH2) to chromosome 2q33 by fluorescence in situ hybridization.";			
RL	Genomics 37:140-141(1996).			
CC	FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.			
CC	TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.			
CC	ALSO EXPRESSED IN THE TESTIS.			
CC	SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; U25128; AAC50157.1; -			
DR	EMBL; U47124; AAA96796.1; -			
DR	EMBL; U47129; AAC50767.1; -			
DR	EMBL; U47125; AAC50767.1; JOINED.			
DR	EMBL; U47126; AAC50767.1; JOINED.			
DR	EMBL; U47127; AAC50767.1; JOINED.			
DR	EMBL; U47128; AAC50767.1; JOINED.			
DR	PIR; A57519; A57519.			
DR	Genew; HGNC:9609; PTHR2.			
DR	MIW; 601469; -			
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.			
DR	GO; GO:0004991; F:parathyroid hormone receptor activity; TAS.			
DR	GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; TAS.			

ALIGNMENTS

P32215 rattus norv
P28217 styela plic
Q13324 homo sapien
P47866 rattus norv
P42784 synchococc
O42603 xenopus lae
P35347 mus musculus
P35353 rattus norv
O62772 ovis aries
O42602 xenopus lae
Q90812 gallus gall
Q60748 mus musculus

34 1.7 523 1 PACR_RAT
35 1.5 117 1 PTH2_STYPL
36 1.5 411 1 CRF2_HUMAN
37 1.5 411 1 CRF2_RAT
38 1.5 411 1 YPEB_SYN2
39 1.5 413 1 CRF2_XENLA
40 1.5 415 1 CRF1_MOUSE
41 1.5 415 1 CRF1_RAT
42 1.5 415 1 CRF1_SHEEP
43 1.5 415 1 CRF1_XENLA
44 1.5 420 1 CRF1_CHICK
45 1.5 431 1 CRF2_MOUSE

FT	DOMAIN	337	355	EXTRACELLULAR (POTENTIAL).
FT	TRANSNEM	356	376	5 (POTENTIAL).
FT	DOMAIN	377	403	CYTOPLASMIC (POTENTIAL).
FT	TRANSNEM	404	422	6 (POTENTIAL).
FT	DOMAIN	423	434	EXTRACELLULAR (POTENTIAL).
FT	TRANSNEM	435	457	7 (POTENTIAL).
FT	DOMAIN	458	585	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	48	114	BY SIMILARITY.
FT	DISULFID	105	145	BY SIMILARITY.
FT	DISULFID	128	167	BY SIMILARITY.
FT	CARBOHYD	148	148	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	163	163	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	173	173	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	585 AA;	65963 MM;	34900384CD6DF477 CRC64;

Query Match 4.6%; Score 25; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.8e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	167	GYPRRLHCTRNTHMHLFVSEMLRA	191
DB	207	GYPRRLHCTRNTHMHLFVSEMLRA	231

RESULT 4

SCRC	HUMAN	STANDARD;	PRT;	440 AA.
ID	SCRC_HUMAN			
AC	P47872; Q12961; Q13213;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Secretin receptor precursor (SCT-R).			
GN	GN			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI	TaxID=9606;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Pancreas;			
RC	MEDLINE=95169147; PubMed=7864894;			
RX	Jiang S., Ulrich C.D.;			
RA	"Molecular cloning and functional expression of a human pancreatic			
RT	secretin receptor.";			
RL	Biochem. Biophys. Res. Commun. 207:883-890(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Pancreas;			
RC	MEDLINE=95336443; PubMed=7612008;			
RX	Chow B.K.-C.;			
RA	"Molecular cloning and functional characterization of a human			
RT	secretin receptor.";			
RL	Biochem. Biophys. Res. Commun. 212:204-211(1995).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Lung;			
RC	MEDLINE=95214632; PubMed=7700244;			
RX	Fatel D.R., Kong Y., Sreedharan S.P.;			
RA	"Genome-wide discovery and analysis of human seven transmembrane helix			
RT	receptor genes.";			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RP	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,			
RA	Tsuteomi S., Aburatani H., Asai K., Akiyama Y.;			
RT	"Genome-wide discovery and analysis of human seven transmembrane helix			
RL	receptor genes.";			
RN	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS			
CC	RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL			
CC	CYCLASE.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS			

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 EMBL; U20178; AAC50106.1; --
 EMBL; U28281; AAA87556.1; --
 EMBL; U13989; AAA64949.1; --
 EMBL; AB065660; BAC05886.1; --
 PIR; JC2532; JC2532.
 Genew; HGNC:10608; SCTR.
 MIM; 182098; --
 GO; GO:0005887; C: integral to plasma membrane; TAS.
 GO; GO:0015055; F: secretin receptor activity; TAS.
 GO; GO:0007586; P: digestion; TAS.
 GO; GO:0007588; P: excretion; TAS.
 GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; TAS.
 InterPro; IPR000832; GPCR secretin.
 InterPro; IPR001879; hormn_receptor.
 Pfam; PF00002; 7tm.2; 1.
 Pfam; PF02793; HRM; 1.
 PRINTS; PR00249; GPCRSECRETIN.
 SMART; SM00008; Hormr; 1.
 PROSITE; PS00649; G PROTEIN RECP F2 1; 1.
 PROSITE; PS00650; G PROTEIN RECP F2 2; 1.
 PROSITE; PS00227; G PROTEIN RECP F2 3; 1.
 PROSITE; PS00261; G PROTEIN RECP F2 4; 1.
 G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 SIGNAL 1 22 POTENTIAL.
 CHAIN 23 440 SECRETIN RECEPTOR.
 DOMAIN 23 143 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 144 167 1 (POTENTIAL).
 DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 175 194 2 (POTENTIAL).
 DOMAIN 195 216 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 217 240 3 (POTENTIAL).
 DOMAIN 241 254 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 255 276 4 (POTENTIAL).
 DOMAIN 277 294 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 295 317 5 (POTENTIAL).
 DOMAIN 318 343 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 344 362 6 (POTENTIAL).
 DOMAIN 363 369 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 370 392 7 (POTENTIAL).
 DOMAIN 393 440 CYTOPLASMIC (POTENTIAL).
 CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 G -> A (IN REF. 1).
 G -> P (IN REF. 2).
 I -> F (IN REF. 3).
 E -> Q (IN REF. 3).
 G -> A (IN REF. 1).
 SEQUENCE 440 AA; 50206 MW; E22CDD0E7C0ACC1 CRC64;
 Query Match 3.5%; Score 19; DB 1; Length 440;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 169 FRELHCTRYNHMLFVSF 187
 |||||
 Db 167 FRELHCTRYNHMLFVSF 185

RESULT 5

SCRC_RAT

ID_SCRC_RAT

STANDARD;

PRT; 449 AA.

AC P23811;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 GN Secretin receptor precursor (SCT-R).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=101116;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=91266890; PubMed=1646711;
 RA Ishihara T., Nakamura S., Kaziro Y., Takahashi T., Takahashi K.,
 RA Nagata S.;
 RT "Molecular cloning and expression of a cDNA encoding the secretin
 receptor";
 RL EMBO J. 10:1635-1641(1991).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CC CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC
 EMBL; X59132; CAA41849.1; --
 PIR; S16319; S16319. GPCR secretin.
 InterPro; IPR000832; GPCR secretin.
 InterPro; IPR001879; hormn_receptor.
 Pfam; PF00002; 7tm.2; 1.
 Pfam; PF02793; HRM; 1.
 PRINTS; PR00249; GPCRSECRETIN.
 SMART; SM00008; Hormr; 1.
 PROSITE; PS00649; G PROTEIN RECP F2 1; 1.
 PROSITE; PS00650; G PROTEIN RECP F2 2; 1.
 PROSITE; PS00227; G PROTEIN RECP F2 3; 1.
 PROSITE; PS00261; G PROTEIN RECP F2 4; 1.
 G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 SIGNAL 1 22 POTENTIAL.
 CHAIN 23 449 SECRETIN RECEPTOR.
 DOMAIN 23 143 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 144 167 1 (POTENTIAL).
 DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 175 194 2 (POTENTIAL).
 DOMAIN 195 216 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 217 240 3 (POTENTIAL).
 DOMAIN 241 254 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 255 276 4 (POTENTIAL).
 DOMAIN 277 294 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 295 317 5 (POTENTIAL).
 DOMAIN 318 343 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 344 362 6 (POTENTIAL).
 DOMAIN 363 369 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 370 392 7 (POTENTIAL).
 DOMAIN 393 449 CYTOPLASMIC (POTENTIAL).
 CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 449 AA; 51234 MW; E70D05B5D061480D CRC64;
 Query Match 3.5%; Score 19; DB 1; Length 449;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

	EMBL; L34610; AAA40011.1; JOINED.	
RC	PIR; I59297; I59297.	
RX	PIR; S44203; S44203.	
RA	HSSP; Q03431; 1BL1.	
RA	MGI; MGI:197801; Pthr1.	
DR	GO; GO:000282; P:bone mineralization; IMP.	
DR	GO; GO:0001501; P:skeletal development; IMP.	
DR	InterPro; IPR000832; GPCR_secretin.	
DR	InterPro; IPR001879; hormn_receptor.	
DR	Pfam; PF00002; 7tm_2; 1.	
DR	Pfam; PF02793; HRM; 1.	
DR	PRINTS; PR00249; GPCRSSECRETIN.	
DR	SMART; SM00008; HORMR; 1.	
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.	
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.	
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.	
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; 1.	
DR	PROSITE; PS02261; G_PROTEIN_RECEP_F2_1; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.	
FT	SIGNAL 1 26	
FT	CHAIN 27 591	
FT	DOMAIN 27 188	
FT	TRANSMEM 189 212	
FT	DOMAIN 213 219	
FT	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 220 239	
FT	DOMAIN 240 282	
FT	TRANSMEM 283 306	
FT	DOMAIN 307 320	
FT	TRANSMEM 321 342	
FT	DOMAIN 343 361	
FT	TRANSMEM 362 382	
FT	DOMAIN 383 409	
FT	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 410 428	
FT	DOMAIN 429 440	
FT	TRANSMEM 441 463	
FT	DOMAIN 464 591	
FT	CYTOPLASMIC (POTENTIAL).	
FT	BY SIMILARITY.	
FT	DISULFID 48 117	
FT	DISULFID 108 148	
FT	DISULFID 131 170	
FT	SEQUENCE 591 AA; 66313 MW; F7876FBD38BDDDFD CRC64;	
QY	Query Match 3.3%; Score 18; DB 1; Length 591;	
Db	Best Local Similarity 100.0%; Pred.No. 4.2e-10;	
Db	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	245 YFLATNYWLVGLYLH 262	
Db	290 YFLATNYWLVGLYLH 307	
RESULT 8	STANDARD; PRT; 591 AA.	
ID	PTRR RAT	
AC	P25961;	
DT	01-MAY-1992 (Rel. 22, Created)	
DT	01-MAY-1992 (Rel. 22, Last sequence update)	
DE	15-SEP-2003 (Rel. 42, Last annotation update)	
DE	Parathyroid hormone/parathyroid hormone-related peptide receptor precursor (PTH/PTHR receptor).	
GN	PTHRI OR PTHRH.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	
OX	NCBI_TaxID=10116;	
RP	SEQUENCE FROM N.A.	

	EMBL; L34610; AAA40011.1; JOINED.	
RC	PIR; I59297; I59297.	
RX	PIR; S44203; S44203.	
RA	HSSP; Q03431; 1BL1.	
RA	MGI; MGI:197801; Pthr1.	
DR	GO; GO:000282; P:bone mineralization; IMP.	
DR	GO; GO:0001501; P:skeletal development; IMP.	
DR	InterPro; IPR000832; GPCR_secretin.	
DR	InterPro; IPR001879; hormn_receptor.	
DR	Pfam; PF00002; 7tm_2; 1.	
DR	Pfam; PF02793; HRM; 1.	
DR	PRINTS; PR00249; GPCRSSECRETIN.	
DR	SMART; SM00008; HORMR; 1.	
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.	
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.	
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.	
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; 1.	
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_5; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.	
FT	SIGNAL 1 26	
FT	CHAIN 27 591	
FT	DOMAIN 27 188	
FT	TRANSMEM 189 212	
FT	DOMAIN 213 219	
FT	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 220 239	
FT	DOMAIN 240 282	
FT	TRANSMEM 283 306	
FT	DOMAIN 307 320	
FT	TRANSMEM 321 342	
FT	DOMAIN 343 361	
FT	TRANSMEM 362 382	
FT	DOMAIN 383 409	
FT	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 410 428	
FT	DOMAIN 429 440	
FT	TRANSMEM 441 463	
FT	DOMAIN 464 591	
FT	CYTOPLASMIC (POTENTIAL).	
FT	BY SIMILARITY.	
FT	DISULFID 48 117	
FT	DISULFID 108 148	
FT	DISULFID 131 170	
FT	SEQUENCE 591 AA; 66313 MW; F7876FBD38BDDDFD CRC64;	
QY	Query Match 3.3%; Score 18; DB 1; Length 591;	
Dd	Best Local Similarity 100.0%; Pred.No. 4.2e-10;	
Db	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	245 YFLATNYWLVLEGLYLH 262	
Db	290 YFLATNYWLVLEGLYLH 307	
RESULT 8	STANDARD; PRT; 591 AA.	
ID	PTRR RAT	
AC	P25961;	
DT	01-MAY-1992 (Rel. 22, Created)	
DT	01-MAY-1992 (Rel. 22, Last sequence update)	
DE	15-SEP-2003 (Rel. 42, Last annotation update)	
DE	Parathyroid hormone/parathyroid hormone-related peptide receptor precursor (PTH/PTHR receptor).	
GN	PTHRI OR PTHRH.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	
OX	NCBI_TaxID=10116;	
RP	[1]	
RP	SEQUENCE FROM N.A.	

FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 591 AA; 66260 MW; 21944F3051B9E9C1 CRC64;

Query Match 3.3%; Score 18; DB 1; Length 591;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|||||
Db 290 YFLATNYWILVEGLYLH 307

RESULT 9
PTTR HUMAN STANDARD; PRT; 593 AA.
AC Q03431;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE Precursor (PTH/PTHrP receptor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RC MEDLINE=93238641; PubMed=8386612;
RA Schipani E., Karga H., Karalis A.C., Potts J.T. Jr., Kronenberg H.M.,
RA Abou-Samra A.-B., Segre G.V., Juppner H.;
RT "Identical complementary deoxyribonucleic acids encode a human renal
RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
RL Endocrinology 132:2157-2165(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RC MEDLINE=93387403; PubMed=8397094;
RA Schneider H., Feyen J.-H., Rao Movva N.;
RT "Cloning and functional expression of a human parathyroid hormone
RT receptor.";
RL Eur. J. Pharmacol. 246:149-155(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95263723; PubMed=7745008;
RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.P.,
RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,
RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,
RA Abou-Samra A.-B., Segre G.V., Juppner H.;
RT "Pseudohypoparathyroidism type 1b is not caused by mutations in the
RT coding exons of the human parathyroid hormone (PTH)/PTH-related
RT peptide receptor gene.";
RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RA Levine M.A.;
RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP EXTRACELLULAR DOMAIN DISULFIDE BONDS.
RX MEDLINE=20374568; PubMed=10913300;
RA Grauschopf U., Lilie H., Honold K., Wozny M., Reusch D., Esswein A.,
RA Schafer W., Rucknagel K.P., Rudolph R.;
RT "The N-terminal fragment of human parathyroid hormone receptor 1
RT constitutes a hormone binding domain and reveals a distinct disulfide
RT pattern.";
RL Biochemistry 39:8878-8887(2000).
RN [6]
RP STRUCTURE BY NMR OF 168-198.

RX MEDLINE=98409426; PubMed=9737850;
RA Pellegrini M., Biello A., Rosenblatt M., Chorev M., Mierke D.F.;
RT "Binding domain of human parathyroid hormone receptor: from
RT conformation to function.";
RL Biochemistry 37:12737-12743(1998).
RN [7]
RP VARIANT MURK-JANSEN ARG-223.
RX MEDLINE=95215874; PubMed=7701349;
RA Schipani E., Kruse K., Juppner H.;
RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type
RT metaphyseal chondrodysplasia.";
RL Science 268:98-100(1995).
RN [8]
RP VARIANTS MURK-JANSEN ARG-223 AND PRO-410.
RX MEDLINE=96366745; PubMed=8703170;
RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
RA Kooh S.W., Cole W.G., Juppner H.;
RT "Constitutively activated receptors for parathyroid hormone and
RT parathyroid hormone-related peptide in Jansen's metaphyseal
RT chondrodysplasia.";
RL New Engl. J. Med. 335:708-714(1996).
RN [9]
RP MUTAGENESIS OF ARG-223 AND PRO-410.
RX MEDLINE=97322091; PubMed=9178745;
RA Schipani E., Jensen G.S., Pincus J., Nissen R.A., Gardella T.J.,
RA Juppner H.;
RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
RT receptors mutated at the two loci for Jansen's metaphyseal
RT chondrodysplasia.";
RL Mol. Endocrinol. 11:851-858(1997).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN
CC KIDNEY, BONE AND LIVER.
CC -!- DISEASE: DEFECTS IN PTHR1 ARE THE CAUSE OF BLOWSTRAND TYPE OF
CC CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA.
CC -!- DISEASE: DEFECTS IN PTHR1 ARE THE CAUSE OF MURK-JANSEN TYPE OF
CC METAPHYSEAL CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA. IT IS
CC A RARE FORM OF SHORT-LIMBED DWARFISM ASSOCIATED WITH HYPERCALCAEMIA
CC AND NORMAL OR LOW SERUM CONCENTRATIONS OF THE TWO PARATHYROID
CC HORMONES.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; I04308; AAA36525.1; -.
CC EMBL; X68596; CAA48589.1; -.
CC EMBL; U22409; AAB60657.1; -.
CC EMBL; U22401; AAB60657.1; JOINED.
CC EMBL; U22402; AAB60657.1; JOINED.
CC EMBL; U22403; AAB60657.1; JOINED.
CC EMBL; U22404; AAB60657.1; JOINED.
CC EMBL; U22405; AAB60657.1; JOINED.
CC EMBL; U22406; AAB60657.1; JOINED.
CC EMBL; U22407; AAB60657.1; JOINED.
CC EMBL; U22408; AAB60657.1; JOINED.
CC EMBL; U17418; AAA56774.1; -.
CC PIR; I38139; A49191.
CC PDB; 1BL1; 30-MAR-99.
CC PDB; 1ET2; 06-SEP-00.
CC PDB; 1ET3; 06-SEP-00.
CC Genew; HGNC:9608; PTHR1.


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RESULT 11
VIPR_CARAU
ID VIPR_CARAU STANDARD; PRT; 447 AA.
AC Q90308;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vasoactive intestinal polypeptide receptor (VIP-R) (VIP receptor).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neoceratognathi; Osteichthyes; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190233; PubMed=90382250;
RA Chow B.K.C., Yuen T.H., Chan K.W.;
RT "Molecular evolution of vertebrate VIP receptors and functional
RT characterization of a VIP receptor from goldfish Carassius auratus.";
RL Gen. Comp. Endocrinol. 105:176-185(1997)
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U56391; A805459.1; -.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G-PROTEIN RECP F2_1; 1.
CC PROSITE; PS00650; G-PROTEIN RECP F2_2; 1.
CC PROSITE; PS00650; G-PROTEIN RECP F2_3; 1.
CC PROSITE; PS00227; G-PROTEIN RECP F2_4; 1.
CC PROSITE; PS00261; G-PROTEIN RECP F2_5; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC DOMAIN 1 103
CC TRANSMEM 104 128
CC DOMAIN 129 135
CC TRANSMEM 136 155
CC DOMAIN 156 178
CC TRANSMEM 179 202
CC DOMAIN 203 216
CC TRANSMEM 217 238
CC DOMAIN 239 256
CC TRANSMEM 257 280
CC DOMAIN 281 305
CC TRANSMEM 306 325
CC DOMAIN 326 337
CC TRANSMEM 338 357
CC DOMAIN 358 447
CC TRANSMEM 447 447
CC CARBOHYD 177 247
CC DISULFID 177 247
CC CARBOHYD 177 247
CC CARBOHYD 22 22
CC CARBOHYD 64 64
CC CARBOHYD 91 91
CC CARBOHYD 169 169
CC SEQUENCE 447 AA; 50959 MW; 66839E243702554C CRC64;
Query Match 3.0%; Score 16; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 172 LHCTRYIHMLFVSP 187
DB 131 LHCTRYIHMLFVSP 146

RESULT 12
GIPR_RAT
ID GIPR_RAT STANDARD; PRT; 455 AA.
AC P43219;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gastric inhibitory polypeptide receptor precursor (GIP-R) (Glucose-
DE dependent insulinotropic polypeptide receptor).
GN GIPR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94062667; PubMed=8243312;
RA Usdin T.B., Mezey E., Button D.C., Brownstein M.J., Bonner T.I.;
RT "Gastric inhibitory polypeptide receptor, a member of the secretin-
RT vasoactive intestinal polypeptide receptor family, is widely distributed
RT in peripheral organs and the brain.";
RL Endocrinology 133:2861-2871(1993).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: PRESENT IN THE PANCREAS AS WELL AS THE GUT.
CC ADIPOSE TISSUE, HEART, PITUITARY, AND INNER LAYERS OF THE ADRENAL
CC CORTEX, WHEREAS IT IS NOT FOUND IN KIDNEY, SPLEEN, OR LIVER. IT IS
CC ALSO EXPRESSED IN SEVERAL BRAIN REGIONS, INCLUDING THE CEREBRAL
CC CORTEX, HIPPOCAMPUS, AND OLFACTORY BULB.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; L19660; AAC37637.1; -.
CC PIR; I53273; I53273.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G-PROTEIN RECP F2_1; 1.
CC PROSITE; PS00650; G-PROTEIN RECP F2_2; 1.
CC PROSITE; PS00227; G-PROTEIN RECP F2_3; 1.
CC PROSITE; PS00261; G-PROTEIN RECP F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 18
CC CHAIN 19 455
CC DOMAIN 19 135
CC TRANSMEM 136 158
CC DOMAIN 159 166
CC TRANSMEM 167 186
CC DOMAIN 187 214
CC TRANSMEM 215 239
CC DOMAIN 240 251
CC TRANSMEM 252 275
CC DOMAIN 276 290
CC TRANSMEM 291 316

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FT DOMAIN 317 338 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 339 359 6 (POTENTIAL).
 FT DOMAIN 360 374 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 375 395 7 (POTENTIAL).
 FT DOMAIN 396 455 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 455 AA; 52256 MW; 5454B0638ABF9A06 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRHCTRNTHM 181
 |||||
 DB 159 FRRHCTRNTHM 171

RESULT 13
 VIPR HUMAN STANDARD; PRT; 457 AA.
 AC P32241; Q15871; DT 01-OCT-1993 (Rel. 27, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE Vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1)
 DE (pituitary adenylate cyclase activating polypeptide type II receptor)
 DE (PACAP type II receptor) (PACAP-R-2).
 GN VIPR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=93290641; PubMed=8390245;
 RA Sreedharan S.P., Patel D.R., Huang J.-X., Goetzl E.J.;
 RT "Cloning and functional expression of a human neuroendocrine
 RT vasoactive intestinal peptide receptor.";
 RL Biochem. Biophys. Res. Commun. 193:546-553(1993).
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Intestine;
 RX MEDLINE=94235025; PubMed=8179610;
 RA Couvineau A., Rouyer-Fessard C., Darmoul D., Maoret J.J., Carrero I.,
 RA Ogier-Denis E., Laburthe M.;
 RT "Human intestinal VIP receptor: cloning and functional expression of
 RT two cDNA encoding proteins with different N-terminal domains.";
 RL Biochem. Biophys. Res. Commun. 200:769-776(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 33-457 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=95001220; PubMed=7917790;
 RA Gagnon A.W., Aiyar N., Elshourbagy N.A.;
 RT "Molecular cloning and functional characterization of a human liver
 RT vasoactive intestinal peptide receptor.";
 RL Cell. Signal. 6:321-333(1994).
 RN [5]
 RP DISULFIDE BOND.
 RX MEDLINE=99126981; PubMed=9928020;
 RA Knudsen S.M., Tams J.W., Wulff B.S., Fahrenkrug J.;
 RT "Importance of conserved cysteines in the extracellular loops of
 RT human PACAP/VIP1 receptor for ligand binding and stimulation of cAMP
 RT production.";

RL Ann. N.Y. Acad. Sci. 865:259-265(1998).
 CC -I- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CC CYCLASE. THE AFFINITY IS VIP = PACAP-27 > PACAP-38.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Short, Synonyms=hIVR8;
 CC IsoId=P32241-1; Sequence=Displayed;
 CC Name=Long, Synonyms=hIVR5;
 CC IsoId=P32241-2; Sequence=VSP_002010;
 CC -I- TISSUE SPECIFICITY: IN LUNG, HF29 COLONIC EPITHELIAL CELLS, RAJI
 CC B-LYMPHOBLASTS. LESSER EXTENT IN BRAIN, HEART, KIDNEY, LIVER AND
 CC PLACENTA.
 CC -I- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; U11087; AAB60362.1; --
 CC EMBL; U11079; AAB60362.1; JOINED.
 CC EMBL; U11080; AAB60362.1; JOINED.
 CC EMBL; U11081; AAB60362.1; JOINED.
 CC EMBL; U11083; AAB60362.1; JOINED.
 CC EMBL; U11084; AAB60362.1; JOINED.
 CC EMBL; U11085; AAB60362.1; JOINED.
 CC EMBL; U11086; AAB60362.1; JOINED.
 CC EMBL; L13288; AAA36805.1; --
 CC EMBL; X77777; CAA54814.1; --
 CC EMBL; X75299; CAA53046.1; --
 CC EMBL; AB065669; BAC05895.1; --
 CC EMBL; L20295; AAA36802.1; --
 CC PIR; JC2194; JC2194.
 CC Genew; HGNC:12694; VIPR1.
 CC MIM; 192321; --
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004999; F:vasoactive intestinal polypeptide receptor . . . ; TAS.
 CC GO; GO:0007586; P:digestion; TAS.
 CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . . ; TAS.
 CC GO; GO:0006955; P:immune response; TAS.
 CC GO; GO:0006936; P:muscle contraction; TAS.
 CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 CC GO; GO:0007268; P:synaptic transmission; TAS.
 CC InterPro; IPR000832; GPCR_secretin.
 CC InterPro; IPR001879; hormn_receptor.
 CC Pfam; PF00002; 7tm_2; 1.
 CC Pfam; PF02793; HRN; 1.
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; Hormr; 1.
 CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 CC PROSITE; PS00627; G_PROTEIN_RECEP_F2_3; 1.
 CC PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Alternative splicing.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 457 VASOACTIVE INTESTINAL POLYPEPTIDE
 FT RECEPTOR 1.
 FT DOMAIN 31 142 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 143 167 1 (POTENTIAL).
 FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 175 194 2 (POTENTIAL).
 FT DOMAIN 195 216 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 217 240 3 (POTENTIAL).
 FT DOMAIN 241 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 276 4 (POTENTIAL).
 FT DOMAIN 277 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 316 5 (POTENTIAL).


```

CC CYCLASE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; U49434; AAA93390.1; -.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G_PROTEIN_RECPT_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECPT_F2_2; 1.
CC PROSITE; PS00227; G_PROTEIN_RECPT_F2_3; 1.
CC PROSITE; PS00261; G_PROTEIN_RECPT_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 31 POTENTIAL.
CC CHAIN 32 458 VASOACTIVE INTESTINAL POLYPEPTIDE
CC RECEPTOR 1.
CC DOMAIN 32 143 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 144 168 1 (POTENTIAL).
CC DOMAIN 169 175 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 176 195 2 (POTENTIAL).
CC DOMAIN 196 217 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 218 241 3 (POTENTIAL).
CC DOMAIN 242 255 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 256 277 4 (POTENTIAL).
CC DOMAIN 278 293 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 294 317 5 (POTENTIAL).
CC DOMAIN 318 342 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 343 362 6 (POTENTIAL).
CC DOMAIN 363 374 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 375 394 7 (POTENTIAL).
CC DOMAIN 395 458 CYTOPLASMIC (POTENTIAL).
CC DISULFID 216 286 BY SIMILARITY.
CC CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 458 AA; 51479 MW; E166E4D6B3BE1189 CRC64;

```

Query Match 2.4%; Score 13; DB 1; Length 458;

Best Local Similarity 100.0%; Pred. No. 4.6e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIHMLF 184

|||||

Db 171 LHCTRYIHMLF 183

Search completed: November 21, 2003, 22:34:29

Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 22:28:00 ; Search time 47 Seconds
(without alignments)
1827.044 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGLSHVWGMLGSL.....DDILMKFSPRPMSPDTEG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	100.0	541	AAW12695	G-protein parathyroid hormone receptor; HLTDG74; parathormone; PTH; calcium; signal transduction; agonist; antagonist; hypocalcaemia; hypophosphataemia; hypoparathyroidism; chronic tetany; osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia; kidney stone; nephrolisis; therapy; diagnosis.
2	363	67.1	550	AAW12695	Human PTH2 seven t
3	363	67.1	550	AAW12695	Lung cancer-associ
4	363	67.1	550	ABP81871	Human parathyroid
5	342	63.2	561	ABUS6731	Lung cancer-associ
6	262	48.4	550	ABUS6386	Non-endogenous hum
7	262	48.4	550	AAW12695	Human PTH2 receptor
8	38	7.0	546	AAW12695	Rat PTH2 receptor
9	25	4.6	515	AAW12695	Opossum kidney PTH

10	25	4.6	515	17	AAW12695	Opossum kidney PTH
11	25	4.6	515	20	AAW12695	Parathyroid hormone
12	25	4.6	515	13	AAW12695	Opossum kidney PTH
13	25	4.6	515	17	AAW12695	Opossum kidney PTH
14	25	4.6	515	20	AAW12695	Parathyroid hormone
15	22	4.1	864	22	ABG27219	Novel human diagno
16	20	3.7	20	24	ABP82552	G protein-coupled
17	19	3.5	440	21	AAW12695	Amino acid sequenc
18	19	3.5	440	22	ABUS6387	Non-endogenous hum
19	19	3.5	440	22	ABUS6387	Human SCRC seven t
20	19	3.5	440	23	ABUS6387	Protein identified
21	19	3.5	440	23	ABUS6387	Human secretin rec
22	19	3.5	440	24	ABP81912	Human secretin rec
23	19	3.5	449	13	AAW12695	Secretin receptor
24	18	3.3	324	18	ABP82551	G protein-coupled
25	18	3.3	324	21	AAW12695	Tethered PTH-1 rec
26	18	3.3	335	21	AAW12695	Tethered PTH-1 rec
27	18	3.3	335	21	AAW12695	Human tethered PTH
28	18	3.3	435	21	AAW12695	A mutant parathyro
29	18	3.3	446	21	AAW12695	Tethered PTH-1 rec
30	18	3.3	448	21	AAW12695	Human tethered PTH
31	18	3.3	450	21	AAW12695	Human tethered PTH
32	18	3.3	536	21	AAW12695	Zebrafish parathyr
33	18	3.3	536	21	AAW12695	Zebrafish PTHR re
34	18	3.3	591	13	AAW12695	Rat bone PTH/PTHrP
35	18	3.3	591	17	AAW12695	Rat bone PTH/PTHrP
36	18	3.3	591	20	AAW12695	Parathyroid hormone
37	18	3.3	593	17	AAW12695	Human kidney PTH/P
38	18	3.3	593	20	AAW12695	Human Parathyroid
39	18	3.3	593	22	ABUS6385	Non-endogenous hum
40	18	3.3	593	22	ABUS6385	Human PTH2 seven t
41	18	3.3	593	24	ABP81872	Human parathyroid
42	18	3.3	595	24	ABG73825	Canine parathyroid
43	18	3.3	614	13	AAW12695	Human kidney PTH/P
44	16	3.0	447	23	ABW79169	Carassius auratus
45	14	2.6	19	13	AAW12695	PTH/PTHrP receptor

ALIGNMENTS

RESULT 1

AAW12695
ID AAW12695 standard; Protein; 541 AA.

XX AC AAW12695;

XX DT 31-MAY-1997 (first entry)

XX DE G-protein parathyroid hormone receptor HLTDG74.

XX KW G-protein parathyroid hormone receptor; HLTDG74; parathormone; PTH; calcium; signal transduction; agonist; antagonist; hypocalcaemia; hypophosphataemia; hypoparathyroidism; chronic tetany; osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia; kidney stone; nephrolisis; therapy; diagnosis.

XX OS Homo sapiens.

XX PN WO9639433-A1.

XX PD 12-DEC-1996.

XX PF 05-JUN-1995; 95WO-US07085.

XX PR 05-JUN-1995; 95WO-US07085.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Li Y, Rosen CA, Ruben SM, Soppet DR;

XX WPI; 1997-043068/04.

XX DR N-PSDB; AAT59619.

XX Human G-protein parathyroid hormone receptor, HLTG74 - used to
PT identify (ant)agonists, used in the treatment of hypo- or
PT hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc
XX
XX Claim 9; Fig 1A-E; 62pp; English.
XX
XX A novel 7-transmembrane receptor (AAW12695) has been identified as a
CC human G-protein parathyroid hormone (PTH) receptor, designated
CC HLTG74. It shows 48.2% homology to the human PTH receptor. Its
CC amino acid sequence was deduced from a cDNA clone (AAT59619) isolated
CC from a human T cell lymphoma tissue cDNA library. Recombinant
CC HLTG74 can be produced in transformed host cells and used to
CC screen for (ant)agonist cpds. Agonists may be used to prevent or
CC treat e.g. hypocalcaemia, hyperphosphatemia, hypoparathyroidism
CC and chronic tetany by stimulating an increase in serum calcium
CC levels. Antagonists can be used to inhibit the receptor e.g. for
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,
CC hypophosphatemia, kidney stone, nephrolithiasis.
XX
XX Sequence 541 AA;
SQ

Query Match 100.0%; Score 541; DB 18; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSLHVGWMLGSCLLARALQSDGTITIEEQIVLVKAKVQCELNITAIQEGE 60
DB 1 MAWLGLSLHVGWMLGSCLLARALQSDGTITIEEQIVLVKAKVQCELNITAIQEGE 60
QY 61 GNCFFPMDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCPNGTWDPMHSLNKTWA 120
DB 61 GNCFFPMDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCPNGTWDPMHSLNKTWA 120
QY 121 NYSDCILRFQPDLSIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNIH 180
DB 121 NYSDCILRFQPDLSIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNIH 180
QY 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVKSOYIGCKIAV 240
DB 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVKSOYIGCKIAV 240
QY 241 VMFIYFLATNYWMLVEGLYLNHLIFVAFSDTKYLMGPFILIGWGPFAAFVAWAVARAT 300
DB 241 VMFIYFLATNYWMLVEGLYLNHLIFVAFSDTKYLMGPFILIGWGPFAAFVAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIMETNAVGHDTKQYRK 360
DB 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIMETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVFVGVHIVFVCLPHSFTGLGWEIRHCELFNFSFQGFVFSIYCYCNGEV 420
DB 361 LAKSTLVLVFVGVHIVFVCLPHSFTGLGWEIRHCELFNFSFQGFVFSIYCYCNGEV 420
QY 421 QAEVKKWSRWNLSDWKETPPCGSRCCSVLTIVTHSTSSQSOVAAAHAWCLSLAKLPR 480
DB 421 QAEVKKWSRWNLSDWKETPPCGSRCCSVLTIVTHSTSSQSOVAAAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLVAMSGVTSQRTASHTLSTRNKEDSGRQDDILMEKPSRPWESNPDT 540
DB 481 SPADSLTATSLVAMSGVTSQRTASHTLSTRNKEDSGRQDDILMEKPSRPWESNPDT 540
QY 541 G 541
DB 541 G 541

RESULT 2
AAB71875
ID AAB71875 standard; Protein; 550 AA.
XX
AC AAB71875;
XX

DT 03-MAY-2001 (first entry)
XX
DE Human PTR2 seven transmembrane domain.
XX
XX
KW Human; PTR2; parathyroid hormone receptor; h15571; immunomodulatory;
KW vascular; hepatic; antiasthma; antimicrobial; antiinflammatory;
KW immunosuppressive; gene therapy; vaccine; G-protein coupled receptor;
KW GPCR; liver fibrosis; respiratory disorder; infection;
KW chronic inflammatory disease; organ-specific autoimmunity;
XX graft rejection; cystic fibrosis.
XX
OS Homo sapiens.
XX
PN WO200109328-A1.
XX
PD 08-FEB-2001.
XX
PP 03-AUG-2000; 2000WO-US21278.
XX
PR 03-AUG-1999; 99US-0146916.
XX 29-FEB-2000; 2000US-0515781.
XX (MILL-) MILLENNIUM PHARM INC.
XX Hodge MR, Lloyd C, Weich NS;
PI
XX WPI; 2001-138653/14.
XX
PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
XX
XX Disclosure; Fig 2; 145pp; English.
XX
CC The present sequence is a human G-protein coupled receptor (GPCR) used
CC for comparison with the seven transmembrane domain of a novel GPCR
CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate GPCR expression. Such diseases includes immune
CC haematological, fibrotic, hepatic and respiratory disorders including
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
CC graft rejection, graft versus host disease, cystic fibrosis and, in
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
CC in the production of antibodies against GPCR and in assays to identify
CC modulators (agonists and antagonists) of GPCR expression and activity.
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
CC used as diagnostic agents for detecting the presence of GPCR
XX polypeptides in samples.
XX
SQ Sequence 550 AA;

Query Match 67.1%; Score 363; DB 22; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LGASHVWGMWMLGSCLLARALQSDGTITIEEQIVLVKAKVQCELNITAIQEGE 63
DB 4 LGASHVWGMWMLGSCLLARALQSDGTITIEEQIVLVKAKVQCELNITAIQEGE 63
QY 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCPNGTWDPMHSLNKTWANS 123
DB 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCPNGTWDPMHSLNKTWANS 123
QY 124 DCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNIHML 183
DB 124 DCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNIHML 183
QY 184 FVSMFLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVKSOYIGCKIAVVMF 243
DB 184 FVSMFLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVKSOYIGCKIAVVMF 243

QY 244 IYFLATNYWILVEGLYHNLIFVAFSDTKVLMGFILGWGPPAFVAAVARATLAD 303
Db 244 IYFLATNYWILVEGLYHNLIFVAFSDTKVLMGFILGWGPPAFVAAVARATLAD 303
QY 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYKRLAK 363
Db 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYKRLAK 363
QY 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRHMCCLFFNSFGQFFVSIYCYCNGEQVQAE 423
Db 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRHMCCLFFNSFGQFFVSIYCYCNGEQVQAE 423
QY 424 VKKWSRWNLSDVWKRTPPCGRRRCGSLVLTVTHTSTSSOSQVAA 467
Db 424 VKKWSRWNLSDVWKRTPPCGRRRCGSLVLTVTHTSTSSOSQVAA 467

RESULT 3

ABU56732
ID ABU56732 standard; Protein; 550 AA.
XX AC ABU56732;
XX DT 02-APR-2003 (first entry)
XX DE Lung cancer-associated polypeptide #325.
XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX OS Unidentified.
XX FN WO200286443-A2.
XX PD 31-OCT-2002.
XX PF 18-APR-2002; 2002WO-US12476.
XX PR 18-APR-2001; 2001US-284770P.
XX PR 10-MAY-2001; 2001US-290492P.
XX PR 09-NOV-2001; 2001US-339245P.
XX PR 13-NOV-2001; 2001US-350666P.
XX PR 29-NOV-2001; 2001US-334370P.
XX PR 12-APR-2002; 2002US-372246P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX PI Aziz N, Murray R;
XX DR WPI; 2003-093161/08.
XX DR N-PSDB; ABX76461.

PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer -
XX
XX Claim 27; Page 439-440; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridises
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung
XX cancer-associated polynucleotides and polypeptides are used for
XX identifying a compound that modulates a lung cancer-associated
XX polypeptide, for inhibiting proliferation of a lung cancer-associated
XX cell to treat lung cancer in a patient and for treating a mammal having
XX lung cancer by administering a modulatory compound identified. The
XX methods are useful for treating lung cancer, such as small cell lung

CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
XX polypeptides of the invention.

SQ Sequence 550 AA;

Query Match 67.1%; Score 363; DB 24; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LGASLHVWGLMLGSLARALQSDGTTTTEEQIVLVKAKVQCELNITAIQLOEGGNC 63
Db 4 LGASLHVWGLMLGSLARALQSDGTTTTEEQIVLVKAKVQCELNITAIQLOEGGNC 63
QY 64 PPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 123
Db 64 PPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 123
QY 124 DCLRFLOPDISIGKQEFERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIHMH 183
Db 124 DCLRFLOPDISIGKQEFERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIHMH 183
QY 184 FVSPMLRATSFVKDVRVVAHIGVKELESIMQDDPONSIEATSDVKSYIGCKTAVVMF 243
Db 184 FVSPMLRATSFVKDVRVVAHIGVKELESIMQDDPONSIEATSDVKSYIGCKTAVVMF 243
QY 244 IYFLATNYWILVEGLYHNLIFVAFSDTKVLMGFILGWGPPAFVAAVARATLAD 303
Db 244 IYFLATNYWILVEGLYHNLIFVAFSDTKVLMGFILGWGPPAFVAAVARATLAD 303
QY 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYKRLAK 363
Db 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYKRLAK 363
QY 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRHMCCLFFNSFGQFFVSIYCYCNGEQVQAE 423
Db 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRHMCCLFFNSFGQFFVSIYCYCNGEQVQAE 423
QY 424 VKKWSRWNLSDVWKRTPPCGRRRCGSLVLTVTHTSTSSOSQVAA 467
Db 424 VKKWSRWNLSDVWKRTPPCGRRRCGSLVLTVTHTSTSSOSQVAA 467

RESULT 4

ABP81871
ID ABP81871 standard; Protein; 550 AA.
XX AC ABP81871;
XX DT 04-MAR-2003 (first entry)
XX DE Human parathyroid hormone receptor 2 protein SEQ ID NO:227.
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX OS Homo sapiens.
XX FN WO200261087-A2.

XX 08-AUG-2002.
 XX 19-DEC-2001; 2001MO-US50107.
 XX 19-DEC-2000; 2000US-257144P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX Burmer GC, Roush CL, Brown JP;
 XX WPI; 2003-046718/04.
 XX N-PSDB; ABZ42718.
 XX
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 XX (GPCR), useful for diagnosing and designing drugs for treating
 XX conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 XX cancer or autoimmune diseases -
 XX
 XX Disclosure; Fig 1; 523pp; English.
 XX
 XX The present invention describes antigenic peptides (I) comprising:
 XX (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 XX acids. Also described: (1) an assay for the detection of a particular
 XX G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 XX and (2) an isolated antibody having high specificity and high affinity
 XX or avidity for a particular GPCR. (1) can be used as GPCR modulators and
 XX in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 XX an antibody against a particular GPCR, and in the production of specific
 XX antibodies. The peptides and antibodies are also useful for detecting the
 XX presence or absence of corresponding GPCRs. The antigenic peptides for
 XX GPCRs and antibodies are useful for diagnosing and designing drugs for
 XX treating immune-related diseases, growth-related diseases, cell
 XX regeneration-related diseases, immunological-related cell proliferative
 XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
 XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
 XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
 XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 XX hypotension renal disorders, rheumatoid arthritis, trauma, ulcers, or
 XX any other disorder in which GPCRs are involved. The antibodies may be
 XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
 XX exemplification of the present invention.
 XX
 XX Sequence 550 AA;
 XX
 XX Query Match 67.1%; Score 363; DB 24; Length 550;
 XX Best Local Similarity 99.8%; Pred. No. 0;
 XX Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 LGASHVWGWLMLGSLARALQSDGTTTIEEQIVLVKAKVQCELNITAQLEGEGNC 63
 DB 4 LGASHVWGWLMLGSLARALQSDGTTTIEEQIVLVKAKVQCELNITAQLEGEGNC 63
 QY 64 PFWDLICWRGTGKTSVPCPPYIYDFNHKGVAFFHGNPNGTDFMHSLNKTWANY 123
 DB 64 PFWDLICWRGTGKTSVPCPPYIYDFNHKGVAFFHGNPNGTDFMHSLNKTWANY 123
 QY 124 DCLRFLOPDISGKQEFERLYVMYTVGYSISFGSLAVAILIIGYFRHLHCTRYNIMHL 183
 DB 124 DCLRFLOPDISGKQEFERLYVMYTVGYSISFGSLAVAILIIGYFRHLHCTRYNIMHL 183
 QY 184 FVSFMLRATSFVKDRVVHAHIGVKELESIMQDDPQNSIEATSVKDSQYIGCKIAVVMF 243
 DB 184 FVSFMLRATSFVKDRVVHAHIGVKELESIMQDDPQNSIEATSVKDSQYIGCKIAVVMF 243
 QY 244 IYFLATNYWILVEGLYHLNLIIVAFPSDTKYLWGLIFGFFAAAFVAAVARATLAD 303
 DB 244 IYFLATNYWILVEGLYHLNLIIVAFPSDTKYLWGLIFGFFAAAFVAAVARATLAD 303

QY 304 ARCWELSAGDIKWIYQAPILAAIGLNFLLNTVVRVLATKIWETNAVGHDTKQYRKLA 363
 DB 304 ARCWELSAGDIKWIYQAPILAAIGLNFLLNTVVRVLATKIWETNAVGHDTKQYRKLA 363
 QY 364 STLVLVLVFGVHYIVFVCLPHSFTGLWEIRMHCELFNSFQGFVSIILYCYNGEVOAE 423
 DB 364 STLVLVLVFGVHYIVFVCLPHSFTGLWEIRMHCELFNSFQGFVSIILYCYNGEVOAE 423
 QY 424 VKKWSRNWLSVDWKRTPPCGSRRCGSLVITVTHSTSSQSOVAA 467
 DB 424 VKKWSRNWLSVDWKRTPPCGSRRCGSLVITVTHSTSSQSOVAA 467

RESULT 5
 ABUS6731
 ID ABUS6731 standard; Protein; 561 AA.
 XX AC ABUS6731;
 XX
 XX 02-APR-2003 (first entry)
 XX
 XX Lung cancer-associated polypeptide #324.
 XX
 XX Lung cancer-associated polypeptide; cytostatic; emphysema;
 XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 XX Unidentified.
 XX
 XX WO200286443-A2.
 XX
 XX 31-OCT-2002.
 XX
 XX 18-APR-2002; 2002WO-US12476.
 XX
 XX 18-APR-2001; 2001US-284770P.
 XX 10-MAY-2001; 2001US-290492P.
 XX 09-NOV-2001; 2001US-339245P.
 XX 13-NOV-2001; 2001US-350666P.
 XX 29-NOV-2001; 2001US-334370P.
 XX 12-APR-2002; 2002US-372246P.
 XX
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX Aziz N, Murray R;
 XX WPI; 2003-093161/08.
 XX N-PSDB; ABX76460.
 XX
 XX Detecting a lung cancer-associated transcript in a cell from a patient
 XX for treating lung cancer, by contacting a biological sample from the
 XX patient with a polynucleotide that exhibits increased or decreased
 XX expression in lung cancer -
 XX
 XX Claim 27; Page 439; 453pp; English.
 XX
 XX The invention relates to a method for detecting a lung cancer-associated
 XX transcript in a cell from a patient, comprising contacting a biological
 XX sample from the patient with a polynucleotide that selectively hybridises
 XX to a sequence that is at least 80 % identical to a gene that exhibits
 XX increased or decreased expression in lung cancer samples. Lung
 XX cancer-associated polynucleotides and polypeptides are used for
 XX identifying a compound that modulates a lung cancer-associated
 XX polypeptide, for inhibiting proliferation of a lung cancer-associated
 XX cell to treat lung cancer in a patient and for treating a mammal having
 XX lung cancer by administering a modulatory compound identified. The
 XX methods are useful for treating lung cancer, such as small cell lung
 XX cancer, non-small cell lung cancer or other benign or precancerous
 XX lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
 XX pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
 XX pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides

KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX Homo sapiens.
 XX WO2000077042-A2.
 XX 21-DEC-2000.
 XX 15-JUN-2000; 2000WO-US16776.
 XX 15-JUN-1999; 99US-0139335.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Usdin TB, Hoare SRJ;
 XX WPI; 2001-122833/13.
 XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX Example 4; Fig I; 106pp; English.
 XX The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC neurotropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cyostatic, antiaesthetic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. The present
 CC sequence represents a PTH2 receptor which is used in the
 CC exemplification of the present invention.
 XX SQ Sequence 550 AA;
 Query Match 48.4%; Score 262; DB 22; Length 550;
 Best Local Similarity 99.6%; Pred. No. 2.1e-259;
 Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 LGASHVWGMVLMGSLARALQSDGTITIEEQIVLVKAKVOCNELNITIAQLQEGGNC 63
 DB 4 LGASHVWGMVLMGSLARALQSDGTITIEEQIVLVKAKVOCNELNITIAQLQEGGNC 63
 QY 64 FPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPGTWDPMHSLNKTWANY 123
 DB 64 FPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPGTWDPMHSLNKTWANY 123
 QY 124 DCLPLQPDISIGQKQFCERLYVMVTVGYSISFSGSLAVAILIIGYFRLHCTRYIHML 183
 DB 124 DCLPLQPDISIGQKQFCERLYVMVTVGYSISFSGSLAVAILIIGYFRLHCTRYIHML 183
 QY 184 FVSFMLRATSFVKDRVHAHIGVKELESIMQDDPQNSIATSVDKSVQIGCKIAVVMF 243
 DB 184 FVSFMLRATSFVKDRVHAHIGVKELESIMQDDPQNSIATSVDKSVQIGCKIAVVMF 243
 QY 244 IYFLATNYWILVEGLYLNHILIFVAFPSDTKYLWGFILMGFPFPAFAVAWAVARATLAD 303
 DB 244 IYFLATNYWILVEGLYLNHILIFVAFPSDTKYLWGFILMGFPFPAFAVAWAVARATLAD 303
 QY 304 ARCWELSGADIKWYIQAPILAAIGNLFILNTVRLATKIWETNAVGHTRKQYKRLAK 363

DB 304 ARCWELSGADIKWYIQAPILAAIGNLFILNTVRLATKIWETNAVGHTRKQYKRLAK 363
 QY 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFQGFVSIICYCNGEVOAE 423
 DB 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFQGFVSIICYCNGEVOAE 423
 QY 424 VKQWMSRWNLSDWKRTPPCGSRRCGSLVLTIVTHSTSSQSQVAA 467
 DB 424 VKQWMSRWNLSDWKRTPPCGSRRCGSLVLTIVTHSTSSQSQVAA 467

RESULT 8

AAB80559
 ID AAB80559 standard; Protein; 546 AA.
 XX AC AAB80559;
 XX 26-APR-2001 (first entry)
 XX Rat PTH2 receptor amino acid sequence.

XX Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; neurotropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
 KW cyostatic; antiaesthetic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.

XX Rattus sp.

XX WO2000077042-A2.

XX 21-DEC-2000.

XX 15-JUN-2000; 2000WO-US16776.

XX 15-JUN-1999; 99US-0139335.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Usdin TB, Hoare SRJ;

XX WPI; 2001-122833/13.

XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -

XX Example 4; Fig I; 106pp; English.

XX The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC neurotropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cyostatic, antiaesthetic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. The present
 CC sequence represents a PTH2 receptor which is used in the
 CC exemplification of the present invention.

XX

SQ Sequence 546 AA;

Query Match 7.0%; Score 38; DB 22; Length 546;
 Best Local Similarity 100.0%; Pred. No. 8.5e-30;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILNTVRVLATKIWTETNAVGHD 353
 |||||
 Db 313 WIYQAPILAAIGLNFILNTVRVLATKIWTETNAVGHD 350

RESULT 9

AAR27704
 ID AAR27704 standard; Protein; 515 AA.

XX AC AAR27704;
 XX 25-MAR-2003 (updated)
 DT 16-MAR-1993 (first entry)

XX Opossum kidney PTH/PTHrP receptor prepd. from clone OK-H.

XX DE Parathyroid hormone; related protein; calcium; antagonist;
 XX KW antibodies; hypercalcaemia.

XX OS Didelphis virginiana.

XX PN WO9217602-A1.

XX PD 15-OCT-1992.

XX PF 06-APR-1992; 92WO-US02821.

XX PR 05-APR-1991; 91US-0681702.

XX PR 06-APR-1992; 92US-0864475.

XX PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
 PI Segre GV;

XX DR N-PSDB; AAQ29604.

XX PT New DNA encoding parathyroid hormone receptor, DNA and antibodies
 PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
 PT and treatment of tumours

XX PS Disclosure; Fig 1; 91pp; English.

XX CC The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
 CC receptor protein sequence was deduced from the DNA sequence of the
 CC clone OK-H, isolated from opossum kidney (OK) cells. The protein
 CC may be used in a therapeutic compsn. to inhibit activation of PTH or
 CC PTHrP and thus reduce the level of calcium in the blood. Cpd.
 CC capable of competing with PTH or PTHrP for binding can be identified
 CC using the protein prod. and DNAs homologous to PTH DNA can be
 CC identified using fragments of the clone as probes. The protein
 CC may be used for the prodn. of antibodies useful for the treatment,
 CC classification, prognosis and/or treatment of disorders related to
 CC the interaction between a cell receptor and a ligand such as in
 CC hypercalcaemia. See also AAR27705-16.
 CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 515 AA;

Query Match 4.6%; Score 25; DB 13; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1.7e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRYNHMLFVSVFLRA 191
 |||||

Db 207 GYFRRLHCTRYNHMLFVSVFLRA 231

RESULT 10

AAR92275
 ID AAR92275 standard; Protein; 515 AA.

XX AC AAR92275;

XX 25-MAR-2003 (updated)

DT 18-MAY-1996 (first entry)

XX DE Opossum kidney PTH/PTHrP receptor.

XX KW Parathyroid hormone; receptor; parathormone; PTH;
 KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
 KW hypercalcaemia; hypocalcaemia; cancer; opossum.

XX OS Didelphis virginiana.

XX PN US5494806-A.

XX PD 27-FEB-1996.

XX PF 06-APR-1992; 92US-0864475.

XX PR 06-APR-1992; 92US-0864475.

XX PR 05-APR-1991; 91US-0681702.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;

XX DR WPI; 1996-139028/14.

XX DR N-PSDB; AAT15945.

XX PT DNA encoding vertebrate parathyroid hormone receptor - useful for
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
 PT cancer etc.

XX PS Claim 1; Fig 1A-1E; 64pp; English.

XX CC Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
 CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
 CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
 CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
 CC separate genes or of a laboratory artifact. The receptor induces an
 CC increase in intracellular cAMP and calcium when challenged with PTH or
 CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
 CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
 CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
 CC Host cells expressing the receptor can be used for diagnostic
 CC measurement of PTH serum levels.
 CC (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 515 AA;

Query Match 4.6%; Score 25; DB 17; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1.7e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRYNHMLFVSVFLRA 191
 |||||

Db 207 GYFRRLHCTRYNHMLFVSVFLRA 231

RESULT 11

AAW73314
 ID AAW73314 standard; Protein; 515 AA.

XX AC AAW73314;

XX DT 08-FEB-1999 (first entry)

XX Parathyroid hormone receptor OK-H.
 XX
 KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
 KW PTH-related hypercalcaemia; opossum.
 XX
 OS Didelphis virginiana.
 XX
 PN US5840853-A.
 XX
 PD 24-NOV-1998.
 XX
 PF 06-JUN-1995; 95US-0471494.
 XX
 PR 06-APR-1992; 92US-0864475.
 PR 05-APR-1991; 91US-0681702.
 PR 06-JUN-1995; 95US-0471494.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX
 PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX
 DR WPI; 1999-034124/03.
 DR N-PSDB; AAV08388.
 XX
 PT Antibody to parathyroid hormone receptor - for diagnostic or
 PT therapeutic use
 XX
 PS Claim 6; Fig 1; 63pp; English.
 XX
 CC This sequence represents the opossum parathyroid hormone (PTH) receptor
 CC OK-H, which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.
 XX
 SQ Sequence 515 AA;
 Query Match 4.6%; Score 25; DB 20; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1.7e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRLHCTRNVIHMLFVSFMLRA 191
 Db 207 GYFRLHCTRNVIHMLFVSFMLRA 231
 RESULT 12
 AAR27705
 ID AAR27705 standard; Protein; 585 AA.
 AC
 XX AAR27705;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-MAR-1993 (first entry)
 XX
 DE Opossum kidney PTH/PTHrP receptor prod. from clone OK-O.
 XX
 KW Parathyroid hormone; related protein; calcium; antagonist;
 KW antibodies; hypercalcaemia.
 XX
 OS Didelphis virginiana.
 XX
 PN WO9217602-A1.
 XX
 PD 15-OCT-1992.
 XX
 PF 06-APR-1992; 92WO-US02821.
 XX
 PR 05-APR-1991; 91US-0681702.
 PR 06-APR-1992; 92US-0864475.

XX
 PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
 XX
 PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
 PI Segre GV;
 XX
 DR WPI; 1992-366271/44.
 DR N-PSDB; AAQ29605.
 XX
 PT New DNA encoding parathyroid hormone receptor, DNA and antibodies
 PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
 PT and treatment of tumours
 XX
 PS Disclosure; Fig 2; 91pp; English.
 XX
 CC The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
 CC receptor protein sequence was deduced from the DNA sequence of the
 CC clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O
 CC is identical to the OK-H clone except at the C-terminal tail as OK-O
 CC encodes a 585 amino acid protein, OK-H encodes one of 515 amino acids.
 CC The difference is attributed to a single nucleotide deleted in the OK-H
 CC sequence causing a frame shift and an earlier stop codon. It is not
 CC known whether OK-O and OK-H represent prods. of two separate genes or
 CC are a laboratory artifact. The protein may be used in a therapeutic
 CC compsn. to inhibit activation of PTH or PTHrP and thus reduce the
 CC level of calcium in the blood. Cpts. capable of competing with PTH
 CC or PTHrP for binding can be identified using the protein prod. and
 CC DNAs homologous to PTH DNA can be identified using fragments of the
 CC clone as probes. The sequence may be used for the prodn. of antibodies
 CC useful for the treatment, classification, prognosis and/or treatment of
 CC disorders related to the interaction between a cell receptor and a
 CC ligand such as in hypercalcaemia. See also AAR27704-16.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 585 AA;
 Query Match 4.6%; Score 25; DB 13; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.9e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRLHCTRNVIHMLFVSFMLRA 191
 Db 207 GYFRLHCTRNVIHMLFVSFMLRA 231
 RESULT 13
 AAR92276
 ID AAR92276 standard; Protein; 585 AA.
 AC
 XX AAR92276;
 XX
 DT 25-MAR-2003 (updated)
 DT 18-MAY-1996 (first entry)
 XX
 DE Opossum kidney PTH/PTHrP receptor.
 XX
 KW Parathyroid hormone; receptor; parathormone; PTH;
 KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
 KW hypercalcaemia; hypocalcaemia; cancer; opossum.
 XX
 OS Didelphis virginiana.
 XX
 PN US5494806-A.
 XX
 PD 27-FEB-1996.
 XX
 PF 06-APR-1992; 92US-0864475.
 XX
 PR 06-APR-1992; 92US-0864475.
 PR 05-APR-1991; 91US-0681702.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX

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OM protein - protein search, using sw model

Run on: November 21, 2003, 22:33:06 ; Search time 21 Seconds
(without alignments)
1090.008 Million cell updates/sec

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Searched: 328717 seqs, 42310858 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1035

Minimum DB seq length: 0
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6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	541	3	US-08-468-011A-2
2	541	100.0	541	4	US-09-236-468A-2
3	541	100.0	541	5	PCT-US95-07085-2
4	60	11.1	60	3	US-08-468-011A-9
5	60	11.1	60	3	US-08-468-011A-11
6	60	11.1	60	3	US-08-468-011A-15
7	60	11.1	60	3	US-08-468-011A-19
8	60	11.1	60	4	US-09-236-468A-9
9	60	11.1	60	4	US-09-236-468A-11
10	60	11.1	60	4	US-09-236-468A-15
11	60	11.1	60	4	US-09-236-468A-19
12	59	10.9	59	3	US-08-468-011A-23
13	59	10.9	59	4	US-09-236-468A-23
14	52	9.6	52	4	US-09-236-468A-13
15	37	6.8	37	3	US-08-468-011A-25
16	37	6.8	37	4	US-09-236-468A-25
17	37	6.8	50	3	US-08-468-011A-13
18	27	5.0	575	4	US-09-449-632-5
19	25	4.6	60	3	US-08-468-011A-20
20	25	4.6	60	4	US-09-236-468A-20
21	25	4.6	515	2	US-08-468-249A-18
22	25	4.6	585	1	US-08-142-439A-6
23	25	4.6	585	2	US-08-142-551B-125
24	25	4.6	585	2	US-08-869-477-6
25	25	4.6	585	2	US-08-468-249A-19
26	21	3.9	21	3	US-08-468-011A-21
27	21	3.9	21	4	US-09-236-468A-21

28	19	3.5	449	1	US-08-142-439A-5	Sequence 5, Appli
29	19	3.5	449	2	US-08-869-477-5	Sequence 5, Appli
30	18	3.3	536	4	US-09-449-632-2	Sequence 2, Appli
31	18	3.3	591	2	US-08-468-249A-20	Sequence 20, Appli
32	18	3.3	593	2	US-08-468-249A-21	Sequence 21, Appli
33	14	2.6	19	1	US-07-864-475A-7	Sequence 7, Appli
34	14	2.6	19	2	US-08-468-249A-7	Sequence 7, Appli
35	14	2.6	60	3	US-08-468-011A-10	Sequence 10, Appli
36	14	2.6	60	4	US-09-236-468A-10	Sequence 10, Appli
37	13	2.4	458	1	US-08-112-817C-2	Sequence 2, Appli
38	13	2.4	1324	2	US-08-811-897A-56	Sequence 56, Appli
39	13	2.4	1324	4	US-09-201-474-56	Sequence 56, Appli
40	12	2.2	445	4	US-09-414-189-1	Sequence 1, Appli
41	11	2.0	542	4	US-09-449-632-4	Sequence 4, Appli
42	10	1.8	10	3	US-08-468-011A-17	Sequence 17, Appli
43	10	1.8	10	4	US-09-236-468A-17	Sequence 17, Appli
44	10	1.8	162	1	US-08-453-956-18	Sequence 18, Appli
45	10	1.8	162	1	US-08-086-631-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-08-468-011A-2
; Sequence 2, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Sopdet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-2

Query Match 100.0%; Score 541; DB 3; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSHVWGLMLGSLRAQSDPTTIEBQIVLVKAKYCCENITAQIQEGE 60
|||||

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Db 1 MAWLGLSLHVGWMLGSCLLARQLDSGTITIEQIVLVULKAKVQCELNITAOQGE 60
QY 61 GNCFFPEWDGLICWPRGTGVKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
Db 61 GNCFFPEWDGLICWPRGTGVKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
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Db 181 MHLFVSFMLRATSI FVKDRVVHAHIGVKELESIMODDPQNSIEATSVKQSYIGCKIAV 240
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Db 241 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLGWFTLIGWGPFAAFVAAWAVARAT 300
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Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVLVFGVHVIVFVCLPHSFTGLGWEIRHCELFNFSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVLVFGVHVIVFVCLPHSFTGLGWEIRHCELFNFSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKQWGRNLSVDWKRTPPCGSRRCGSVLTVTHTSTSSQVAAAHAHAWCLSLAKLPR 480
Db 421 QAEVKQWGRNLSVDWKRTPPCGSRRCGSVLTVTHTSTSSQVAAAHAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKPSRPWESNPDT 540
Db 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKPSRPWESNPDT 540
QY 541 G 541
Db 541 G 541

RESULT 2
US-09-236-468A-2
; Sequence 2, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTGDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-2

Query Match 100.0%; Score 541; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSLHVGWMLGSCLLARQLDSGTITIEQIVLVULKAKVQCELNITAOQGE 60
Db 1 MAWLGLSLHVGWMLGSCLLARQLDSGTITIEQIVLVULKAKVQCELNITAOQGE 60
QY 61 GNCFFPEWDGLICWPRGTGVKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
Db 61 GNCFFPEWDGLICWPRGTGVKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
QY 121 NYSDCRLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIH 180
Db 121 NYSDCRLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIH 180
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Db 121 NYSDCRLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIH 180
QY 181 MHLFVSFMLRATSI FVKDRVVHAHIGVKELESIMODDPQNSIEATSVKQSYIGCKIAV 240
Db 181 MHLFVSFMLRATSI FVKDRVVHAHIGVKELESIMODDPQNSIEATSVKQSYIGCKIAV 240
QY 241 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLGWFTLIGWGPFAAFVAAWAVARAT 300
Db 241 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLGWFTLIGWGPFAAFVAAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVLVFGVHVIVFVCLPHSFTGLGWEIRHCELFNFSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVLVFGVHVIVFVCLPHSFTGLGWEIRHCELFNFSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKQWGRNLSVDWKRTPPCGSRRCGSVLTVTHTSTSSQVAAAHAHAWCLSLAKLPR 480
Db 421 QAEVKQWGRNLSVDWKRTPPCGSRRCGSVLTVTHTSTSSQVAAAHAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKPSRPWESNPDT 540
Db 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKPSRPWESNPDT 540
QY 541 G 541
Db 541 G 541

RESULT 3
PCT-US95-07085-2
; Sequence 2, Application PC/TUS9507085
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
; TITLE OF INVENTION: HLTGDG74
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESS: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07085
; FILING DATE: 05-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-393
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07085-2
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Query Match 100.0%; Score 541; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSHVHWGLMGLSCLLARAQLDSGTITIEQIVLVKAKVQCELNITTAQORGE 60
DB 1 MAWLGLSHVHWGLMGLSCLLARAQLDSGTITIEQIVLVKAKVQCELNITTAQORGE 60
QY 61 GNCFFPBDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNCTWDFHSLNKTTWA 120
DB 61 GNCFFPBDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNCTWDFHSLNKTTWA 120
QY 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGVSYISFGSLAVAILIIGYFRRLHCTRNYYH 180
DB 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGVSYISFGSLAVAILIIGYFRRLHCTRNYYH 180
QY 181 MHLFVGFMLEATSI FVKDRVVHAHIGVKELESIMODDPQNSTEATSVDKSOYIGCKIAV 240
DB 181 MHLFVGFMLEATSI FVKDRVVHAHIGVKELESIMODDPQNSTEATSVDKSOYIGCKIAV 240
QY 241 VMFIYFLATNYWILVEGLYHLNLI FVAFFSDTKYLMGFILIGWGPFAAFVAAMAVARAT 300
DB 241 VMFIYFLATNYWILVEGLYHLNLI FVAFFSDTKYLMGFILIGWGPFAAFVAAMAVARAT 300
QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKINETNAVGHDTKQYRK 360
DB 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKINETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVFVGVHVI FVCLPHSTFTGLGWEIRMECELFNFNSFQGFVSIICYNGEV 420
DB 361 LAKSTLVLVFVGVHVI FVCLPHSTFTGLGWEIRMECELFNFNSFQGFVSIICYNGEV 420
QY 421 QAEVKKQMSRWNLSDVWKRTPPCGSRRCGSLVTVTTHSTSSQSOQAAAHAWCLSLAKLPR 480
DB 421 QAEVKKQMSRWNLSDVWKRTPPCGSRRCGSLVTVTTHSTSSQSOQAAAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKSRPMESNPDT 540
DB 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKSRPMESNPDT 540
QY 541 G 541
DB 541 G 541

RESULT 4
US-08-468-011A-9
; Sequence 9, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-11

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYWILVEGLYHLNLI FVAFFSDT 273
DB 1 IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYWILVEGLYHLNLI FVAFFSDT 60

RESULT 5
US-08-468-011A-11
; Sequence 11, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-11

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 274 KYLWGFILGWGPFAAFAVAWAVARATLADARCWELSGADIKWYQAPILAAIGLNFILF 333
 Db 1 KYLWGFILGWGPFAAFAVAWAVARATLADARCWELSGADIKWYQAPILAAIGLNFILF 60

RESULT 6

US-08-468-011A-15
 ; Sequence 15, Application US/08468011A
 ; Patent No. 6030804
 ; GENERAL INFORMATION:
 ; APPLICANT: Soppet, Daniel R
 ; APPLICANT: Yi, Li
 ; APPLICANT: Rosen, Craig A
 ; APPLICANT: Ruben, Steven
 ; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
 ; TITLE OF INVENTION: HLTG74
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
 ; ADDRESSEE: Stewart & Olstein
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07068-1739

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/468,011A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MULLINS, J.G.
 ; REGISTRATION NUMBER: 33,073
 ; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 60 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-468-011A-15

Query Match 11.1%; Score 60; DB 3; Length 60;
 Best Local Similarity 100.0%; Pred. No. 4.2e-49;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 EGNCFPEWDLGICWPRGTGKISAVPCPYIYDFNHKGVAFRHCNPGTWDPMHSLNKTW 119
 Db 1 EGNCFPEWDLGICWPRGTGKISAVPCPYIYDFNHKGVAFRHCNPGTWDPMHSLNKTW 60

RESULT 7

US-08-468-011A-19
 ; Sequence 19, Application US/08468011A
 ; Patent No. 6030804
 ; GENERAL INFORMATION:
 ; APPLICANT: Soppet, Daniel R
 ; APPLICANT: Yi, Li
 ; APPLICANT: Rosen, Craig A
 ; APPLICANT: Ruben, Steven
 ; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
 ; TITLE OF INVENTION: HLTG74
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,

ADDRESSEE: Stewart & Olstein
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: NJ
 COUNTRY: USA
 ZIP: 07068-1739
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/468,011A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MULLINS, J.G.
 ; REGISTRATION NUMBER: 33,073
 ; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 60 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-468-011A-19

Query Match 11.1%; Score 60; DB 3; Length 60;
 Best Local Similarity 100.0%; Pred. No. 4.2e-49;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 KOEFCERLYVMYTVGYSISFGSLAVAILIIGFRLHCTRNVIHMLFVSEMLRATSI FV 196
 Db 1 KOEFCERLYVMYTVGYSISFGSLAVAILIIGFRLHCTRNVIHMLFVSEMLRATSI FV 60

RESULT 8

US-09-236-468A-9
 ; Sequence 9, Application US/09236468A
 ; Patent No. 6338951
 ; GENERAL INFORMATION:
 ; APPLICANT: Soppet et al.
 ; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
 ; FILE REFERENCE: PF201D1
 ; CURRENT APPLICATION NUMBER: US/09/236,468A
 ; CURRENT FILING DATE: 1999-01-25
 ; PRIOR FILING DATE: 1999-01-25
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 60
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-236-468A-9

Query Match 11.1%; Score 60; DB 4; Length 60;
 Best Local Similarity 100.0%; Pred. No. 4.2e-49;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 IMQDDPQNSIATSVDSQYIGCKIAVVMFYFLATNYTWLVREGLYLNLI FVAFPSDT 273
 Db 1 IMQDDPQNSIATSVDSQYIGCKIAVVMFYFLATNYTWLVREGLYLNLI FVAFPSDT 60

RESULT 9

US-09-236-468A-11
 ; Sequence 11, Application US/09236468A
 ; Patent No. 6338951
 ; GENERAL INFORMATION:

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; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTGDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-11

Query Match      11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 KYLWGFILGWGFPAAFAVAAVARATLADARCWELSGADIKWYQADILAAIGINFLIF 333
Db 1 KYLWGFILGWGFPAAFAVAAVARATLADARCWELSGADIKWYQADILAAIGINFLIF 60

RESULT 10
US-09-236-468A-15
; Sequence 15, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTGDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-15

Query Match      11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTW 119
Db 1 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTW 60

RESULT 11
US-09-236-468A-19
; Sequence 19, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTGDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-19
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Query Match      11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 KQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIHMLFVSEMLRATSI 196
Db 1 KQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIHMLFVSEMLRATSI 60

RESULT 12
US-08-468-011A-23
; Sequence 23, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTGDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-23

Query Match      10.9%; Score 59; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.6e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 TGLGWEIRMEHCELFENSFOGFFVSIYCYCNQGEVQAEVKQWSRWNLSDVWKETPCGS 445
Db 1 TGLGWEIRMEHCELFENSFOGFFVSIYCYCNQGEVQAEVKQWSRWNLSDVWKETPCGS 59

RESULT 13
US-09-236-468A-23
; Sequence 23, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTGDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
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; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-23

Query Match 10.9%; Score 59; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.6e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 387 TGLGWEIRMHCELFNFSGFVSIYCYCNGEYQAEVKQWGRWNLSDVWKRTPPCGS 445
Db 1 TGLGWEIRMHCELFNFSGFVSIYCYCNGEYQAEVKQWGRWNLSDVWKRTPPCGS 59

RESULT 14
US-09-236-468A-13
; Sequence 13, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-13

Query Match 9.6%; Score 52; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3e-41;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 334 LNTVRVLATKIWEINAVGHDRKQYRKLAKSTLVLVFVGVHYIVFVCLPHS 55
Db 1 LNTVRVLATKIWEINAVGHDRKQYRKLAKSTLVLVFVGVHYIVFVCLPHS 52

RESULT 15
US-08-468-011A-25
; Sequence 25, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Oistein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-25

Query Match 6.8%; Score 37; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 24 AQLDSGDTITIEEQIVLVKAKVQCELNITLAQLQEGE 60
Db 1 AQLDSGDTITIEEQIVLVKAKVQCELNITLAQLQEGE 37

Search completed: November 21, 2003, 22:36:28
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 22:35:26 ; Search time 36 Seconds
(without alignments)

2743.463 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGLSHVWGLMLGSL.....DDILMERKSPRMESNPDTG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 666188 seqs, 182559486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 3255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	363	67.1	550	15	US-10-225-567A-227
2	262	48.4	550	12	US-09-826-509-565
3	216	39.9	550	15	US-10-014-162-110
4	33	6.1	546	15	US-10-014-162-109
5	27	5.0	575	12	US-10-372-095-5
6	25	4.6	515	12	US-10-267-730-18
7	25	4.6	585	12	US-10-267-730-19
8	20	3.7	20	15	US-10-225-567A-1225
9	19	3.5	353	12	US-10-017-161-696
10	19	3.5	440	12	US-09-826-509-567
11	19	3.5	440	15	US-10-225-567A-310
12	18	3.3	18	15	US-10-225-567A-1224
13	18	3.3	536	12	US-10-372-095-2
14	18	3.3	591	10	US-09-943-446-7
15	18	3.3	591	10	US-09-943-446-8

16	18	3.3	591	12	US-10-267-730-20
17	18	3.3	593	10	US-09-943-446-9
18	18	3.3	593	12	US-10-267-730-21
19	18	3.3	593	12	US-09-826-509-563
20	18	3.3	593	15	US-10-225-567A-229
21	18	3.3	595	10	US-09-943-446-6
22	18	3.3	964	12	US-10-017-161-710
23	14	2.6	19	12	US-10-267-730-7
24	13	2.4	457	15	US-09-826-509-579
25	13	2.4	457	15	US-10-225-567A-469
26	13	2.4	1324	10	US-09-935-371-56
27	12	2.2	368	9	US-09-796-338A-19
28	12	2.2	288	12	US-10-145-586-19
29	12	2.2	268	15	US-10-282-837-19
30	12	2.2	271	9	US-09-795-693-36
31	12	2.2	271	15	US-10-156-239-36
32	12	2.2	271	15	US-10-199-485-36
33	12	2.2	466	12	US-10-241-220-78
34	12	2.2	466	12	US-09-826-509-507
35	12	2.2	466	15	US-10-225-567A-128
36	11	2.0	542	12	US-10-372-095-4
37	10	1.8	11	10	US-09-966-871-62
38	10	1.8	11	14	US-10-039-645-62
39	10	1.8	11	15	US-10-139-084-62
40	10	1.8	273	15	US-10-120-604-11
41	10	1.8	477	14	US-10-010-085-6
42	10	1.8	477	15	US-10-225-567A-134
43	10	1.8	553	15	US-10-225-567A-520
44	9	1.7	10	10	US-09-966-871-67
45	9	1.7	10	14	US-10-039-645-67

ALIGNMENTS

RESULT 1

US-10-225-567A-227

; Sequence 227, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burner, Glenn C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 227

; LENGTH: 550

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-227

Query Match 67.1%; Score 363; DB 15; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LGASLHVWGLMLGSCLLARQLDSGTITIEQIVLVKAKVQCELNITAIQLOEGGNC 63

Db 4 LGASLHVWGLMLGSCLLARQLDSGTITIEQIVLVKAKVQCELNITAIQLOEGGNC 63

QY 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRCNPNGTWDFMHSLNKTKWNTS 123

Db 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRCNPNGTWDFMHSLNKTKWNTS 123

QY 124 DCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYPRRLHCTNYHML 183

Db 124 DCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYPRRLHCTNYHML 183

QY 184 FVSMPLRATSI FVKDRVVAHIGVKELESIMQDPONSIEATSVDSQYIGCKIAVMF 243
 Db 184 FVSMPLRATSI FVKDRVVAHIGVKELESIMQDPONSIEATSVDSQYIGCKIAVMF 243
 QY 244 IYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFILGWGPPAFAVAWAVARATLAD 303
 Db 244 IYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFILGWGPPAFAVAWAVARATLAD 303
 QY 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTRKQYRKLAK 363
 Db 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTRKQYRKLAK 363
 QY 364 STLVLVVFGVHYIVFVCLPHSFTGLGWEIRMCCELFFNSFQGFVSIYCYCNGEVOAE 423
 Db 364 STLVLVVFGVHYIVFVCLPHSFTGLGWEIRMCCELFFNSFQGFVSIYCYCNGEVOAE 423
 QY 424 VKQWRSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAA 467
 Db 424 VKQWRSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAA 467

RESULT 2

US-09-826-509-565
 ; Sequence 565, Application US/09826509
 ; Publication No. US20030204073A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lehmann-Bruinema, Karin
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
 ; TITLE OF INVENTION: Protein-Coupled Receptors
 ; FILE REFERENCE: AREN-207
 ; CURRENT APPLICATION NUMBER: US/09/826,509
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: 09/170,496
 ; PRIOR FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: PatentIn Version 2.1
 ; SEQ ID NO 565
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-826-509-565

Query Match 48.4%; Score 262; DB 12; Length 550;
 Best Local Similarity 99.6%; Pred. No. 5.9e-250; Indels 0; Gaps 0;
 Matches 462; Conservative 0; Mismatches 2

QY 4 LGASLHVGMWMLGSCLLARAQLDSGTITIEBQIVLVKAKYQCELNITAOQ-GEQGN 63
 Db 4 LGASLHVGMWMLGSCLLARAQLDSGTITIEBQIVLVKAKYQCELNITAOQ-GEQGN 63
 QY 64 PPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPGTDFHSLNKTWANY 123
 Db 64 PPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPGTDFHSLNKTWANY 123
 QY 124 DCLRFLOPDISIGKOEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNTHMHL 183
 Db 124 DCLRFLOPDISIGKOEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNTHMHL 183
 QY 184 FVSMPLRATSI FVKDRVVAHIGVKELESIMQDPONSIEATSVDSQYIGCKIAVMF 243
 Db 184 FVSMPLRATSI FVKDRVVAHIGVKELESIMQDPONSIEATSVDSQYIGCKIAVMF 243
 QY 244 IYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFILGWGPPAFAVAWAVARATLAD 303
 Db 244 IYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFILGWGPPAFAVAWAVARATLAD 303
 QY 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTRKQYRKLAK 363

Db 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTRKQYRKLAK 363
 QY 364 STLVLVVFGVHYIVFVCLPHSFTGLGWEIRMCCELFFNSFQGFVSIYCYCNGEVOAE 423
 Db 364 SPLVLVLFVFGVHYIVFVCLPHSFTGLGWEIRMCCELFFNSFQGFVSIYCYCNGEVOAE 423
 QY 424 VKQWRSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAA 467
 Db 424 VKQWRSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAA 467

RESULT 3

US-10-014-162-110
 ; Sequence 110, Application US/10014162
 ; Publication No. US20030032096A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Usdin, Ted B.
 ; APPLICANT: Hoare, Samuel R.J.
 ; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
 ; FILE REFERENCE: NIH175.001C1
 ; CURRENT APPLICATION NUMBER: US/10/014,162
 ; CURRENT FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/1677
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/139335
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 110
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-014-162-110

Query Match 39.9%; Score 216; DB 15; Length 550;
 Best Local Similarity 100.0%; Pred. No. 1.6e-204; Indels 0; Gaps 0;
 Matches 216; Conservative 0; Mismatches 0

QY 252 YWILVEGLYLNLI FVAFPSDTKYLWGFILGWGPPAFAVAWAVARATLADARCWELSA 311
 Db 252 YWILVEGLYLNLI FVAFPSDTKYLWGFILGWGPPAFAVAWAVARATLADARCWELSA 311
 QY 312 GDIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLV 371
 Db 312 GDIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLV 371
 QY 372 FGVHYIVFVCLPHSFTGLGWEIRMCCELFFNSFQGFVSIYCYCNGEVOAEVKQWRSW 431
 Db 372 FGVHYIVFVCLPHSFTGLGWEIRMCCELFFNSFQGFVSIYCYCNGEVOAEVKQWRSW 431
 QY 432 NLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAA 467
 Db 432 NLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAA 467

RESULT 4

US-10-014-162-109
 ; Sequence 109, Application US/10014162
 ; Publication No. US20030032096A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Usdin, Ted B.
 ; APPLICANT: Hoare, Samuel R.J.
 ; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
 ; FILE REFERENCE: NIH175.001C1
 ; CURRENT APPLICATION NUMBER: US/10/014,162
 ; CURRENT FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/1677
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/139335
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 109


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; LENGTH: 546
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(546)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-014-162-109

Query Match          6.1%; Score 33; DB 15; Length 546;
Best Local Similarity 100.0%; Pred. No. 9.3e-24; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 0;

QY 148 YTVGYSISFGSLAVAILIIGYFRLHCTRNYYH 180
Db 146 YTVGYSISFGSLAVAILIIGYFRLHCTRNYYH 178

RESULT 5
US-10-372-095-5
; Sequence 5, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubil, David A.
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-5

Query Match          5.0%; Score 27; DB 12; Length 575;
Best Local Similarity 100.0%; Pred. No. 8.2e-18; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;

QY 165 IIGYFRLHCTRNYYIHMLFVFSFMLRA 191
Db 193 IIGYFRLHCTRNYYIHMLFVFSFMLRA 219

RESULT 6
US-10-267-730-18
; Sequence 18, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-18
```

```
US-10-267-730-18

Query Match          4.6%; Score 25; DB 12; Length 515;
Best Local Similarity 100.0%; Pred. No. 7e-16; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 167 GYFRLHCTRNYYIHMLFVFSFMLRA 191
Db 207 GYFRLHCTRNYYIHMLFVFSFMLRA 231

RESULT 7
US-10-267-730-19
; Sequence 19, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-19

Query Match          4.6%; Score 25; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.9e-16; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 167 GYFRLHCTRNYYIHMLFVFSFMLRA 191
Db 207 GYFRLHCTRNYYIHMLFVFSFMLRA 231

RESULT 8
US-10-225-567A-1225
; Sequence 1225, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1225
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1225

Query Match          3.7%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e-12; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 211 ESLIMQDDPQNSIATSVDK 230
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Db 1 ESLIMQDDPQNSIEATSVDK 20
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RESULT 9
US-10-017-161-696
; Publication No. US20030143666A1
; Sequence 696, Application US/10017161
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ASURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 696
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-696
Query Match 3.5%; Score 19; DB 12; Length 353;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNHYHMLFVSF 187
|||||
Db 23 FRLHCTRNHYHMLFVSF 41
|||||

RESULT 10
US-09-826-509-567
; Publication No. US20030204073A1
; Sequence 567, Application US/09826509
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 567
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-567
Query Match 3.5%; Score 19; DB 12; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNHYHMLFVSF 187
|||||
Db 167 FRLHCTRNHYHMLFVSF 185
|||||

RESULT 11
US-10-225-567A-310
; Publication No. US20030113798A1
; Sequence 310, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 310
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-310
Query Match 3.5%; Score 19; DB 15; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNHYHMLFVSF 187
|||||
Db 167 FRLHCTRNHYHMLFVSF 185
|||||

RESULT 12
US-10-225-567A-1224
; Publication No. US20030113798A1
; Sequence 1224, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1224
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1224
Query Match 3.3%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 KAKVQCELNITAQLEGE 60
|||||
Db 1 KAKVQCELNITAQLEGE 18
|||||

RESULT 13
US-10-372-095-2
; Publication No. US20030162256A1
; Sequence 2, Application US/10372095
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRN
; ORGANISM: Danio rerio
US-10-372-095-2

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Query Match 3.3%; Score 18; DB 12; Length 536;
Best Local Similarity 100.0%; Pred. No. 6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels

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RESULT 14
US-09-943-446-7
; Sequence 7, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Binong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGRP
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus No. US20020146777A1vegicus
US-09-943-446-7

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Query Match 3.3%; Score 18; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
US-09-943-446-8
; Sequence 8, Application US/09943446
; Patent No. US2002014677A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: FC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 591
;

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; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-943-446-8

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Query Match 3.3%; Score 18; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels

Search completed: November 21, 2003, 22:40:59
Job time : 37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:31:46 ; Search time 39 Seconds
(without alignments)
3579.653 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGAHVGWMLGSL.....DDLMEKSPMESNPDTG 541

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 6

Total number of hits satisfying chosen parameters: 4788

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL.23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	363	67.1	621	Q8N429	Q8N429 homo sapien
2	38	7.0	169	Q9R1P4	Q9R1P4 mus musculus
3	38	7.0	237	Q8BUM8	Q8BUM8 mus musculus
4	38	7.0	546	Q91V95	Q91V95 mus musculus
5	27	5.0	575	Q3PWB7	Q3PWB7 brachydanio
6	20	3.7	94	Q3PRG1	Q3PRG1 ictalurus p
7	19	3.5	528	Q81V17	Q81V17 homo sapien
8	18	3.3	333	Q8NSV1	Q8NSV1 homo sapien
9	18	3.3	536	Q3PVP3	Q3PVP3 brachydanio
10	18	3.3	591	Q91VW4	Q91VW4 mus musculus
11	18	3.3	595	Q9TU31	Q9TU31 canis fami
12	18	3.3	964	Q8NHB4	Q8NHB4 homo sapien
13	16	3.0	419	Q8AXV3	Q8AXV3 fugu rubrip
14	13	2.4	418	Q9IBG2	Q9IBG2 gallus gall
15	13	2.4	444	Q9YHC6	Q9YHC6 rana ridibu
16	13	2.4	459	Q9J140	Q9J140 mus musculus

17	11	2.0	542	13	Q9PVD2	Q9PVD2 brachydanio
18	10	1.8	48	11	Q9JIY4	Q9JIY4 mus musculus
19	10	1.8	167	13	Q9YHC8	Q9YHC8 rana ridibu
20	10	1.8	227	4	Q8WUR8	Q8WUR8 homo sapien
21	9	1.7	31	13	Q98TU4	Q98TU4 brachydanio
22	9	1.7	202	13	Q98955	Q98955 meleagris g
23	9	1.7	374	6	Q8WNR0	Q8WNR0 ovis aries
24	9	1.7	402	6	Q8WNR0	Q8WNR0 ovis aries
25	9	1.7	419	13	Q8AXV4	Q8AXV4 fugu rubrip
26	9	1.7	459	11	Q8BGA4	Q8BGA4 mus musculus
27	9	1.7	455	13	Q73769	Q73769 carassius a
28	9	1.7	485	11	Q8K0B5	Q8K0B5 mus musculus
29	9	1.7	496	11	Q8BLT3	Q8BLT3 mus musculus
30	9	1.7	589	6	Q9GMD1	Q9GMD1 cryptotlagus
31	8	1.5	37	4	Q8WXR5	Q8WXR5 homo sapien
32	8	1.5	126	13	Q57671	Q57671 meleagris g
33	8	1.5	168	13	Q9YHC7	Q9YHC7 rana ridibu
34	8	1.5	304	11	Q8EM22	Q8EM22 mus musculus
35	8	1.5	379	2	Q8RM00	Q8RM00 acinetobact
36	8	1.5	405	13	Q98UC1	Q98UC1 ameiliurus ne
37	8	1.5	410	6	Q8WML9	Q8WML9 tupaiia bela
38	8	1.5	414	13	Q8AWA1	Q8AWA1 oncorhynch
39	8	1.5	415	6	Q9BGU4	Q9BGU4 bos taurus
40	8	1.5	415	6	Q8WNR0	Q8WNR0 tupaiia bela
41	8	1.5	415	11	Q8K3R2	Q8K3R2 mesocricetu
42	8	1.5	428	13	Q98UC0	Q98UC0 ameiliurus ne
43	8	1.5	430	13	Q8AWA2	Q8AWA2 oncorhynch
44	8	1.5	437	6	Q8WML8	Q8WML8 tupaiia bela
45	8	1.5	438	13	Q73768	Q73768 carassius a

ALIGNMENTS

RESULT 1

Q8N429 PRELIMINARY; PRT; 621 AA.
AC Q8N429; 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Parathyroid hormone receptor 2 (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036811; AAH36811.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM_1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
FT NON TER 1 1
SQ SEQUENCE 621 AA; 62929 MW; 8B0A5A84899436D2 CRC64;

Query Match 67.1%; Score 363; DB 4; Length 621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 LGASLHVWGMVLMGSCLLARAQLDSGTTITBEQIVLVKAKVQCENITAQLOEGGNC 63

Db 75 LGASLHVWGMVLMGSCLLARAQLDSGTTITBEQIVLVKAKVQCENITAQLOEGGNC 134

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QY 64 FPEWDGLI CWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTWANYS 123
DB 135 FPEWDGLI CWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTWANYS 194
QY 124 DCLFLOPDISIGKOECEBLYMYTVGVYSISFGSLAVALLIIGYFRRLHCTRNHYHML 183
DB 195 DCLFLOPDISIGKOECEBLYMYTVGVYSISFGSLAVALLIIGYFRRLHCTRNHYHML 254
QY 184 FVSPMLRATSI FVXDRVVAHIGVKELESIMQDDPONSIEATSDVKSQYIGCKIAVWVF 243
DB 255 FVSPMLRATSI FVXDRVVAHIGVKELESIMQDDPONSIEATSDVKSQYIGCKIAVWVF 314
QY 244 IYFLATNYWTLVBEGLYHNLIFVAFPSDTKYLWGFLLIGWGPFAAFVAWAVARATLAD 303
DB 315 IYFLATNYWTLVBEGLYHNLIFVAFPSDTKYLWGFLLIGWGPFAAFVAWAVARATLAD 374
QY 304 ARCWELSGADIKWYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDRKQYKRLAK 363
DB 375 ARCWELSGADIKWYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDRKQYKRLAK 434
QY 364 STLVLVLFVGHYIVFVCLPHSFTGLGWELRMHCELFNSFOGFFVSIYCYCNGEVOAE 423
DB 435 STLVLVLFVGHYIVFVCLPHSFTGLGWELRMHCELFNSFOGFFVSIYCYCNGEVOAE 494
QY 424 VKQWWSRWNLSDVMKRTPPCGSRRCGSLVLTVTHTSTSSQSQVAA 467
DB 495 VKQWWSRWNLSDVMKRTPPCGSRRCGSLVLTVTHTSTSSQSQVAA 538

RESULT 2
Q9R1D4 PRELIMINARY; PRT; 169 AA.
AC Q9R1D4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Parathyroid hormone type-2 receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
RT parathyroid hormone and not by human or teleost parathyroid hormone-
RT related peptide. Implications for the evolutionary conservation of
RT calcium-regulating peptide hormones."
RL J. Biol. Chem. 274:23035-23042 (1999).
DR EMBL; AF132083; AAD51909.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PSS0261; G_PROTEIN_RECEP_F2_4; 1.
FT NON TER 1
FT NON TER 169
SQ SEQUENCE 169 AA; 19674 MW; 748CC8231F1C69EA CRC64;

Query Match 7.0%; Score 38; DB 11; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.9e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDR 353
DB 66 WIYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDR 103

RESULT 3
Q9BUM8 PRELIMINARY; PRT; 237 AA.
AC Q9BUM8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Parathyroid hormone receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK083278; BAC38840.1; -.
FT NON TER 1
FT NON TER 237
SQ SEQUENCE 237 AA; 26863 MW; FA35AC19C1FF5257 CRC64;

Query Match 7.0%; Score 38; DB 11; Length 237;
Best Local Similarity 100.0%; Pred. No. 3.9e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDR 353
DB 4 WIYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDR 41

RESULT 4
Q91V95 PRELIMINARY; PRT; 546 AA.
AC Q91V95;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Parathyroid hormone receptor.
GN PTHR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS, and ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikeia J.M.;
RT "High-throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AF32078; AAK56106.1; -.
DR EMBL; AF32077; AAK56105.1; -.
DR EMBL; AK045576; BAC32420.1; -.
DR MGD; MGI:2180917; Pthr2.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; HormR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

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DR PROSITE; P850227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; P850261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 546 AA; 61908 MW; 628051EF181A1DF3 CRC64;

Query Match 7.0%; Score 38; DB 11; Length 546;
Best Local Similarity 100.0%; Pred. No. 8.2e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILNTVRVLATKIWNNAVGH 353
DB 313 WIYQAPILAAIGLNFILNTVRVLATKIWNNAVGH 350

RESULT 5
Q9PWB7
ID Q9PWB7 PRELIMINARY; PRT; 575 AA.
AC Q9PWB7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Parathyroid hormone type-2 receptor.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
parathyroid hormone and not by human or teleost parathyroid hormone-
related peptide. Implications for the evolutionary conservation of
calcium-regulating peptide hormones.";
RL J. Biol. Chem. 274:23035-23042(1999).
DR EMBL; AF132082; AAD51906.1; -.
DR EMBL; AF132078; AAD51906.1; JOINED.
DR EMBL; AF132079; AAD51906.1; JOINED.
DR EMBL; AF132080; AAD51906.1; JOINED.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm 2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 94 94
SQ SEQUENCE 94 AA; 10729 MW; D949182B1D2613EF CRC64;

Query Match 3.7%; Score 20; DB 13; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 FIYFLATNYWILVEGLYLH 262
DB 10 FIYFLATNYWILVEGLYLH 29

RESULT 7
Q8IV17
ID Q8IV17 PRELIMINARY; PRT; 528 AA.
AC Q8IV17;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to secretin receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035757; AAH35757.1; -.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 528 528
SQ SEQUENCE 528 AA; 58944 MW; 6AFEE299E1A76BC2 CRC64;

Query Match 3.5%; Score 19; DB 4; Length 528;
Best Local Similarity 100.0%; Pred. No. 8.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNVIHMLFVSF 187
DB 255 FRRLHCTRNVIHMLFVSF 273

RESULT 8
Q8NSV1
ID Q8NSV1 PRELIMINARY; PRT; 333 AA.
AC Q8NSV1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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Query Match	3.3%;	Score 18;	DB 13;	Length 536;	
Best Local Similarity	100.0%;	Pred. No. 9.9e-10;			
Matches	18;	Conservative	0;	Mismatches	0; Gaps 0;
QY	167	GYFRLHCTRNYYHMLF	184		
DB	167	GYFRLHCTRNYYHMLF	184		
RESULT 10					
Q91WV4		PRELIMINARY;	PRT;	591 AA.	
ID	Q91WV4				
AC	Q91WV4;				
DT	01-DEC-2001 (TrEMBLrel. 19, Created)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)				
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)				
DE	Parathyroid hormone receptor.				
GN	PTHr.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RA	Strausberg R.;				
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC013446; AAH13446.1; -				
DR	MED; MGI:97801; Pthr.				
DR	InterPro; IPR000832; GPCR_secretin.				
DR	InterPro; IPR001879; hormn_receptor.				
DR	Pfam; PF00002; 7tm_2; 1.				
DR	Pfam; PF02793; HRM; 1.				
DR	PRINTS; PR00249; GPCRSECRETIN.				
DR	SMART; SM00008; HormR; 1				
DR	PROSITE; PS00649; G_PROTEIN_REC_P2_1; 1.				
DR	PROSITE; PS00650; G_PROTEIN_REC_P2_2; 1.				
DR	PROSITE; PS50227; G_PROTEIN_REC_P2_3; 1.				
DR	PROSITE; PS50261; G_PROTEIN_REC_P2_4; 1.				
KW	Receptor.				
SQ	SEQUENCE	591 AA;	66361 MW;	5E29CF63E5BAFED CRC64;	
Query Match	3.3%;	Score 18;	DB 11;	Length 591;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-09;			
Matches	18;	Conservative	0;	Mismatches	0; Gaps 0;
QY	245	YFLATNYYWILVGLYLH	262		
DB	290	YFLATNYYWILVGLYLH	307		
RESULT 11					
Q9TU31		PRELIMINARY;	PRT;	595 AA.	
ID	Q9TU31				
AC	Q9TU31;				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DT	01-OCT-2001 (TrEMBLrel. 18, Last annotation update)				
DE	Parathyroid hormone receptor-1.				
GN	PTH1.				
OS	Canis familiaris (Dog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
OX	NCBI_TaxID=9615;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RA	Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;				
RT	"Molecular cloning and functional characterization of the canine				
RT	parathyroid hormone receptor-1 (PTH1).";				
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF167095; AAD55938.1; -				
DR	HSSP; Q03431; 1BL1.				

DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 595 AA; 66308 MW; 09568ECF38D4D258 CRC64;

Query Match 3.3%; Score 18; DB 6; Length 595;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|||||
DB 289 YFLATNYWILVEGLYLH 306

RESULT 12

Q8NHB4 PRELIMINARY; PRT; 964 AA.
AC Q8NHB4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB065462; BAC05721.1; -.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 3.
DR Pfam; PF02793; HRM; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 964 AA; 105706 MW; 8EA72B44244DFD5D CRC64;

Query Match 3.3%; Score 18; DB 4; Length 964;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|||||
DB 564 YFLATNYWILVEGLYLH 581

RESULT 13

Q8AXV3 PRELIMINARY; PRT; 419 AA.
AC Q8AXV3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vasoactive intestinal peptide receptor 1 A.
GN VIPR1A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]

RP SEQUENCE FROM N.A.
RA Cardoso J.C.R., Power D.M., Canario A.V.M., Elgar G., Clark M.S.;
RT "Isolation and characterisation of the VIPR/PACAP receptor gene family
in Fugu rubripes";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296144; CAC82588.1; -.
KW Receptor.
SQ SEQUENCE 419 AA; 47607 MW; F21C006AA4E1B698 CRC64;

Query Match 3.0%; Score 16; DB 13; Length 419;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMLFVSF 187
|||||
DB 130 LHCTRNYIHMLFVSF 145

RESULT 14

Q9IBG2 PRELIMINARY; PRT; 418 AA.
AC Q9IBG2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Vasoactive intestinal peptide receptor (Fragment).
GN CVIPR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21218647; PubMed=11319166;
RA Kanaku N., Shimada K., Ohkubo T., Saito N., Suzuki T., Matsuda Y.,
RA Zadowory D.;
RT "Molecular cloning of chicken vasoactive intestinal polypeptide
receptor complementary DNA, tissue distribution and chromosomal
localization."
RL Biol. Reprod. 64:1575-1581(2001).
DR EMBL; AB029895; BAA95164.1; -.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 418 AA; 48191 MW; 7AE4796ADCB08FF3 CRC64;

Query Match 2.4%; Score 13; DB 13; Length 418;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMLF 184
|||||
DB 130 LHCTRNYIHMLF 142

RESULT 15

Q9YHC6 PRELIMINARY; PRT; 444 AA.
ID Q9YHC6
AC Q9YHC6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Vasoactive intestinal peptide/pituitary adenylate cyclase activating
 DE polypeptide receptor.
 OS Rana ridibunda (laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 CX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=99165178; PubMed=10067855;
 RA Alexandre D., Ancuar Y., Jegou S., Fournier A., Vaudry H.;
 RT "A cloned frog vasoactive intestinal polypeptide/pituitary adenylate
 RT cyclase-activating polypeptide receptor exhibits pharmacological and
 RT tissue distribution characteristics of both VPAC1 and VPAC2 receptors
 RT in mammals.";
 RL Endocrinology 140:1285-1293(1999).
 DR EMBL; AF100644; AAD03602.1; -.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HormR; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 SQ SEQUENCE 444 AA; 50955 MW; 883B35B729314C4C CRC64;

Query Match 2.4%; Score 13; DB 13; Length 444;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRYIHMLF 184
 |||||
 Db 157 LHCTRYIHMLF 169

Search completed: November 21, 2003, 22:35:21
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 22:21:14 ; Search time 46 Seconds
(without alignments)
1866.763 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 2907

Sequence: 1 MAWLGASLHWGWLQSL.....DDILMEKPSRMESNPDTG 541

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2907	100.0	541	AAW12695	G-protein parathyroid hormone receptor; HLTDG74; parathormone; PTH; calcium; signal transduction; agonist; antagonist; hypocalcaemia; hyperphosphataemia; hypoparathyroidism; chronic tetany; osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia; kidney stone; nephrolithiasis; therapy; diagnosis.
2	2635	90.6	550	AAW12695	Human sapiens.
3	2635	90.6	550	AAW12695	Human sapiens.
4	2635	90.6	550	AAW12695	Human sapiens.
5	2629	90.4	550	AAW12695	Human sapiens.
6	2626	90.3	550	AAW12695	Human sapiens.
7	2513	86.4	561	AAW12695	Human sapiens.
8	2217.5	76.3	546	AAW12695	Human sapiens.
9	1418.5	48.8	536	AAW12695	Human sapiens.

10	1418.5	48.8	536	21	AAW12695	Zebrafish PTH1 re
11	1392	47.9	585	17	AAW12695	Opossum kidney PTH
12	1392	47.9	585	20	AAW12695	Parathyroid hormone
13	1391	47.9	585	13	AAW12695	Opossum kidney PTH
14	1388	47.7	515	17	AAW12695	Opossum kidney PTH
15	1388	47.7	515	20	AAW12695	Parathyroid hormone
16	1375	47.3	515	13	AAW12695	Opossum kidney PTH
17	1345.5	46.3	595	24	ABG73825	Canine parathyroid
18	1336.5	46.0	593	22	AAW12695	Human PTH seven t
19	1336.5	46.0	593	24	ABP81872	Human parathyroid
20	1331.5	45.8	591	17	AAW12695	Rat bone PTH/PTHrP
21	1331.5	45.8	591	20	AAW12695	Parathyroid hormone
22	1331.5	45.8	593	20	AAW12695	Human parathyroid
23	1330.5	45.8	593	22	ABW56385	Non-endogenous hum
24	1323.5	45.5	591	13	AAW12695	Rat bone PTH/PTHrP
25	1313	45.2	593	17	AAW12695	Human kidney PTH/p
26	1307.5	45.0	542	21	AAW12695	Zebrafish parathyr
27	1303.5	44.8	614	13	AAW12695	Human kidney PTH/p
28	1302.5	44.8	523	21	AAW12695	Zebrafish PTH3R re
29	1043	35.9	448	21	AAW12695	Human tethered PTH
30	1043	35.9	450	21	AAW12695	Human tethered PTH
31	1041	35.8	435	21	AAW12695	Human tethered PTH
32	1038	35.7	446	21	AAW12695	Tethered PTH-1 rec
33	1036	35.6	435	21	AAW12695	A mutant parathyro
34	1007.5	34.7	335	21	AAW12695	Tethered PTH-1 rec
35	1005.5	34.6	324	21	AAW12695	Tethered PTH-1 rec
36	814	28.0	444	23	ABW79165	Rana ridibunda VPA
37	801	27.6	449	13	AAW12695	Secretin receptor.
38	791.5	27.2	459	23	ABW79165	Mouse VPAC1 rece
39	785	27.0	458	16	AAW12695	Porcine vasoactive
40	785	27.0	458	23	ABW79165	Porcine VPAC1 rece
41	785	27.0	458	23	ABW79165	Porcine VPAC1 rece
42	784	27.0	440	22	AAW12695	Human SCRC seven t
43	784	27.0	440	23	ABW1877	Protein identified
44	784	27.0	440	23	ABW1877	Human secretin rec
45	784	27.0	440	24	ABP81912	Human secretin rec

ALIGNMENTS

RESULT 1

AAW12695

ID AAW12695 standard; Protein; 541 AA.

AC AAW12695;

XX

DT 31-MAY-1997 (first entry)

XX

DE G-protein parathyroid hormone receptor HLTDG74.

XX

KW G-protein parathyroid hormone receptor; HLTDG74; parathormone; PTH; calcium; signal transduction; agonist; antagonist; hypocalcaemia; hyperphosphataemia; hypoparathyroidism; chronic tetany; osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia; kidney stone; nephrolithiasis; therapy; diagnosis.

KW

XX

OS Homo sapiens.

XX

PN W09639433-A1.

XX

PD 12-DEC-1996.

XX

PF 05-JUN-1995; 95WO-US07085.

XX

PR 05-JUN-1995; 95WO-US07085.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Li Y, Rosen CA, Ruben SM, Soppet DR;

XX

DR WPI; 1997-043068/04.

XX

DR N-PSDB; AAT59619.

XX Human G-protein parathyroid hormone receptor, HLTG74 - used to
PT identify (ant)agonists, used in the treatment of hypo- or
PT hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc
XX
XX Claim 9; Fig 1A-E; 62pp; English.
XX
XX A novel 7-transmembrane receptor (AAW12695) has been identified as a
CC human G-protein parathyroid hormone (PTH) receptor, designated
CC HLTG74. It shows 48.2% homology to the human PTH receptor. Its
CC amino acid sequence was deduced from a cDNA clone (AAW59619) isolated
CC from a human T cell lymphoma tissue cDNA library. Recombinant
CC HLTG74 can be produced in transfected host cells and used to
CC screen for (ant)agonist cpds. Agonists may be used to prevent or
CC treat e.g. hypocalcaemia, hyperphosphataemia, hypoparathyroidism
CC and chronic tetany by stimulating an increase in serum calcium
CC levels. Antagonists can be used to inhibit the receptor e.g. for
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,
CC hypophosphataemia, kidney stone, nephrolisis.
XX
XX Sequence 541 AA;
XX
XX Query Match 100.0%; Score 2907; DB 18; Length 541;
XX Best Local Similarity 100.0%; Pred. No. 8.1e-307;
XX Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAWLGLSLHVMGLMGLSCLLARAQLDSGTTTIEEQIVLVKAKVQCELNITAQLOEGE 60
XX Db 1 MAWLGLSLHVMGLMGLSCLLARAQLDSGTTTIEEQIVLVKAKVQCELNITAQLOEGE 60
XX QY 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNGTWDPMHSLNKTTWA 120
XX Db 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNGTWDPMHSLNKTTWA 120
XX QY 121 NYSDCLRFLOPDISIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
XX Db 121 NYSDCLRFLOPDISIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
XX QY 181 MHLFVSEMLRATSIYFKDRVVAHIGVKELESIMQDDPONSIEATSVKSYIGCKIAV 240
XX Db 181 MHLFVSEMLRATSIYFKDRVVAHIGVKELESIMQDDPONSIEATSVKSYIGCKIAV 240
XX QY 241 VMFIYFLATNYWILVEGLYHLNLIYVAFPSDTKYLWGFILIGWFPFAFVAWAVARAT 300
XX Db 241 VMFIYFLATNYWILVEGLYHLNLIYVAFPSDTKYLWGFILIGWFPFAFVAWAVARAT 300
XX QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYRK 360
XX Db 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYRK 360
XX QY 361 LAKSTLVLVFGVHHYIVFVCLPHSFTGLGWEIRMECELFNFSFGFFVSIYCYCNGEV 420
XX Db 361 LAKSTLVLVFGVHHYIVFVCLPHSFTGLGWEIRMECELFNFSFGFFVSIYCYCNGEV 420
XX QY 421 QAEVKQWGRNLSVDWKKTPPCGSRRCGSLVLTVTHTSSQSQVAHAHAWCLSLAKLPR 480
XX Db 421 QAEVKQWGRNLSVDWKKTPPCGSRRCGSLVLTVTHTSSQSQVAHAHAWCLSLAKLPR 480
XX QY 481 SPADSLTATSLYLAMSGVTQSRFASHTLSTRNKEDSGRQDDILMEKSRPMESNPDT 540
XX Db 481 SPADSLTATSLYLAMSGVTQSRFASHTLSTRNKEDSGRQDDILMEKSRPMESNPDT 540
XX QY 541 G 541
XX Db 541 G 541
XX
XX RESULT 2
XX AAB71875
XX ID AAB71875 standard; Protein; 550 AA.
XX AC
XX AAB71875;
XX

DT 03-MAY-2001 (first entry)
XX Human PTH2 seven transmembrane domain.
XX
XX Human; PTH2; parathyroid hormone receptor; h15571; immunomodulatory;
XX vascular; hepatic; antiasthma; antimicrobial; antiinflammatory;
XX immunosuppressive; gene therapy; vaccine; G-protein coupled receptor;
XX GPCR; liver fibrosis; respiratory disorder; infection;
XX chronic inflammatory disease; organ-specific autoimmunity;
XX graft rejection; cystic fibrosis.
XX
XX Homo sapiens.
XX
XX WO200109328-A1.
XX
XX 08-FEB-2001.
XX
XX 03-AUG-2000; 2000WO-US21278.
XX
XX 03-AUG-1999; 99US-0146916.
XX 29-FEB-2000; 2000US-0515781.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Hodge MR, Lloyd C, Weich NS;
XX
XX WPI; 2001-138653/14.
XX
XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
XX for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
XX
XX Disclosure; Fig 2; 145pp; English.
XX
XX The present sequence is a human G-protein coupled receptor (GPCR) used
XX for comparison with the seven transmembrane domain of a novel GPCR
XX designated h15571. h15571 GPCR polynucleotides and polypeptides may be
XX used in the prevention, treatment and diagnosis of diseases associated
XX with inappropriate GPCR expression. Such diseases includes immune,
XX haematological, fibrotic, hepatic and respiratory disorders including
XX asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
XX infections, chronic inflammatory diseases, organ-specific autoimmunity,
XX graft rejection, graft versus host disease, cystic fibrosis and, in
XX particular, liver fibrosis. The GPCR polypeptides may be used as antigens
XX in the production of antibodies against GPCR and in assays to identify
XX modulators (agonists and antagonists) of GPCR expression and activity.
XX The anti-GPCR antibodies and GPCR antagonists may also be used to down
XX regulate GPCR expression and activity. The anti-GPCR antibodies may be
XX used as diagnostic agents for detecting the presence of GPCR
XX polypeptides in samples.
XX
XX Sequence 550 AA;
XX
XX Query Match 90.6%; Score 2635; DB 22; Length 550;
XX Best Local Similarity 91.4%; Pred. No. 3.3e-277;
XX Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;
XX
XX QY 1 MAWLGLSLHVMGLMGLSCLLARAQLDSGTTTIEEQIVLVKAKVQCELNITAQLOEGE 60
XX Db 1 MAWLGLSLHVMGLMGLSCLLARAQLDSGTTTIEEQIVLVKAKVQCELNITAQLOEGE 60
XX QY 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNGTWDPMHSLNKTTWA 120
XX Db 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNGTWDPMHSLNKTTWA 120
XX QY 121 NYSDCLRFLOPDISIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
XX Db 121 NYSDCLRFLOPDISIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
XX QY 181 MHLFVSEMLRATSIYFKDRVVAHIGVKELESIMQDDPONSIEATSVKSYIGCKIAV 240
XX Db 181 MHLFVSEMLRATSIYFKDRVVAHIGVKELESIMQDDPONSIEATSVKSYIGCKIAV 240

QY 241 VMFIYFLATNYWILVEGLYLHNLIFVAFESDTKYLWGFIILGWGFPAAFAVAWAVARAT 300
D 241 VMFIYFLATNYWILVEGLYLHNLIFVAFESDTKYLWGFIILGWGFPAAFAVAWAVARAT 300
QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDRKQYRK 360
D 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDRKQYRK 360
QY 361 LAKSTLVLVFVGHVYIVFVCLPHSFTGLGWEIRMHCELPFNSFQGFVSIYCYNGEV 420
D 361 LAKSTLVLVFVGHVYIVFVCLPHSFTGLGWEIRMHCELPFNSFQGFVSIYCYNGEV 420
QY 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL---SLAK 477
D 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL---SLAK 480
QY 478 LPRSPADSLTATSLYKAMSGVTQSRFASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
D 481 IASRQFDS-----HITLPGYVWNSQEQCLPHSFHEETKEDSGRQDDILMEKPSRPM 534
QY 535 SNPDTEG 541
D 535 SNPDTEG 541

RESULT 3
ABU56732
ID ABU56732 standard; Protein; 550 AA.
XX AC ABU56732;
XX
DT 02-APR-2003 (first entry)
DE Lung cancer-associated polypeptide #325.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US12476.
XX
PR 18-APR-2001; 2001US-284770P.
PR 10-MAY-2001; 2001US-290492P.
PR 09-NOV-2001; 2001US-339245P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-NOV-2001; 2001US-334370P.
PR 12-APR-2002; 2002US-372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX WPI; 2003-093161/08.
DR N-PSDB; ABX76461.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer -
XX
PS Claim 27; Page 439-440; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises

CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
CC polypeptides of the invention.
XX
SQ Sequence 550 AA;
Query Match 90.6%; Score 2635; DB 24; Length 550;
Best Local Similarity 91.4%; Pred. No. 3.3e-277;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;
QY 1 MAWLGLASLHVWGLMLGSCLLARAOQDSGTITIEEQIVLVKAKVQCELNITAOQEGE 60
D 1 MAGLGLASLHVWGLMLGSCLLARAOQDSGTITIEEQIVLVKAKVQCELNITAOQEGE 60
QY 61 GNCFFPEWDGLICWPRGTGVKISAVPCPPYIYDFNKHGVAFRHCPNPGTDFHSLNKTWA 120
D 61 GNCFFPEWDGLICWPRGTGVKISAVPCPPYIYDFNKHGVAFRHCPNPGTDFHSLNKTWA 120
QY 121 NYSDCLRFLOPDISIGKQBFCERLYVMYTVGVYSISFGSLAVAILIIGYFRLHCTRYIH 180
D 121 NYSDCLRFLOPDISIGKQBFCERLYVMYTVGVYSISFGSLAVAILIIGYFRLHCTRYIH 180
QY 181 MELFVSFMLRATSIKORVVAHIGVKELESIMQDDPQNSIEATSVKQYIGCKIAV 240
D 181 MELFVSFMLRATSIKORVVAHIGVKELESIMQDDPQNSIEATSVKQYIGCKIAV 240
QY 241 VMFIYFLATNYWILVEGLYLHNLIFVAFESDTKYLWGFIILGWGFPAAFAVAWAVARAT 300
D 241 VMFIYFLATNYWILVEGLYLHNLIFVAFESDTKYLWGFIILGWGFPAAFAVAWAVARAT 300
QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDRKQYRK 360
D 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDRKQYRK 360
QY 361 LAKSTLVLVFVGHVYIVFVCLPHSFTGLGWEIRMHCELPFNSFQGFVSIYCYNGEV 420
D 361 LAKSTLVLVFVGHVYIVFVCLPHSFTGLGWEIRMHCELPFNSFQGFVSIYCYNGEV 420
QY 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL---SLAK 477
D 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL---SLAK 480
QY 478 LPRSPADSLTATSLYKAMSGVTQSRFASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
D 481 IASRQFDS-----HITLPGYVWNSQEQCLPHSFHEETKEDSGRQDDILMEKPSRPM 534
QY 535 SNPDTEG 541
D 535 SNPDTEG 541
RESULT 4
ABP81871
ID ABP81871 standard; Protein; 550 AA.
XX AC ABP81871;
XX
DT 04-MAR-2003 (first entry)
DE Human parathyroid hormone receptor 2 protein SEQ ID NO:227.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

XX Homo sapiens.

OS WO200261087-A2.

PN 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US50107.

XX 19-DEC-2000; 2000US-257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

PI Burmer GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

DR N-PSDB; ABZ42718.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42859 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 550 AA;

Query Match 90.6%; Score 2635; DB 24; Length 550;

Best Local Similarity 91.4%; Pred. No. 3.3e-277;

Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

QY 1 MAMLGASLHVWGLMGLSCLLARQLDSDGTITIERQIVLVLRKAKVQCELNITAIQEQE 60

DB 1 MAGLGASLHVWGLMGLSCLLARQLDSDGTITIERQIVLVLRKAKVQCELNITAIQEQE 60

QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPNGTWDFMELSKNTWA 120
 DB 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPNGTWDFMELSKNTWA 120
 QY 121 NYSDCLRFLOPDISIGKQFCERLYMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYYH 180
 DB 121 NYSDCLRFLOPDISIGKQFCERLYMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYYH 180
 QY 181 MHLFVSMFLRATSIYFKVDRVVAHIGVKELESIMODDPONSTEATSVDSQYIGCKIAV 240
 DB 181 MHLFVSMFLRATSIYFKVDRVVAHIGVKELESIMODDPONSTEATSVDSQYIGCKIAV 240
 QY 241 VMFIYFLATNYWMLVEGLYLNLIIFVAFSDTKYLWGFILIGWGFPAFVAAWAVARAT 300
 DB 241 VMFIYFLATNYWMLVEGLYLNLIIFVAFSDTKYLWGFILIGWGFPAFVAAWAVARAT 300
 QY 301 LADARCWELSAGDIKWYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDTTRQYRK 360
 DB 301 LADARCWELSAGDIKWYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDTTRQYRK 360
 QY 361 LAKSTLVLVFVGVHYIVFVCLPHSFTHGLWEIRHCELFNFNSFQGFVSIYYCNGEV 420
 DB 361 LAKSTLVLVFVGVHYIVFVCLPHSFTHGLWEIRHCELFNFNSFQGFVSIYYCNGEV 420
 QY 421 QAEVKQWGRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAAAHAWCL---SLAK 477
 DB 421 QAEVKQWGRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAAAHAWCL---SLAK 480
 QY 478 LPRSPADSLTATSLYLAMSGVTQSRPTASHLS---TRSNKEDSGRQRDDILMEKPRPME 534
 DB 481 IASRQPDSD-----HITLPGYVMSNEQDCLPHSFHEETKEDSGRQDDILMEKPRPME 534
 QY 535 SNPDTEG 541
 DB 535 SNPDTEG 541
 RESULT 5
 ABB56386
 ID ABB56386 standard; Protein; 550 AA.
 XX
 AC ABB56386;
 XX
 DT 18-FEB-2002 (first entry)
 DE Non-endogenous human GPCR protein, SEQ ID NO: 565.
 XX
 KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 XX constitutively activated GPCR; agonist; disease.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200177172-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 05-APR-2001; 2001WO-US11098.
 XX
 PR 07-APR-2000; 2000US-195747P.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Lehmann-Bruinsma K, Liaw CW, Lin I;
 XX
 DR WPI; 2001-648759/74.
 DR N-PSDB; ABI98022.
 XX
 PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with
 PT versions of GPCRs -
 XX
 PS Claim 1; Page 367-369; 394pp; English.

XX CC The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous
 CC constitutively activated versions of known GPCRs are used in the
 CC invention for the direct identification of candidate compounds as
 CC receptor agonists, inverse agonists or partial agonists. Such
 CC agonists are useful as therapeutic agents for diseases or disorders
 CC associated with GPCRs. The present sequence is a non-endogenous
 CC version of a known human GPCR.
 XX SQ Sequence 550 AA;

Query Match 90.4%; Score 2629; DB 22; Length 550;
 Best Local Similarity 91.2%; Pred. No. 1.5e-276;
 Matches 499; Conservative 6; Mismatches 30; Indels 12; Gaps 3;

QY 1 MAWLGLSHVWGMLMGLSCLLARALQSDGTTIERQIVLVKAKVQCELNITAIQOE 60
 DB 1 MAGLGASLHVWGMLMGLSCLLARALQSDGTTIERQIVLVKAKVQCELNITAIQOE 60

QY 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNK 120
 DB 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNK 120

QY 121 NYSDCLRFLOPDISIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTENY 180
 DB 121 NYSDCLRFLOPDISIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTENY 180

QY 181 MHLFVSFMLRATSIYFKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQVIGCKIAV 240
 DB 181 MHLFVSFMLRATSIYFKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQVIGCKIAV 240

QY 241 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLMGFFILGWGPPAFVAWAARAT 300
 DB 241 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLMGFFILGWGPPAFVAWAARAT 300

QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDRKQYRK 360
 DB 301 LADARCWELSGADIKWIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDRKQYRK 360

QY 361 LAKSTLVLVFVGHVYIVFVCLPHSTGLGWEIRHMCLEFFNSFQGFVSIYCYCNQEV 420
 DB 361 LAKSPVLVLFVGHVYIVFVCLPHSTGLGWEIRHMCLEFFNSFQGFVSIYCYCNQEV 420

QY 421 QAEVKQWRNLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQVAHAACWCL---SLAK 477
 DB 421 QAEVKQWRNLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQVAHAACWCL---SLAK 477

QY 478 LPRSPADSLTATSLYLAMSGVTQSRRTASHTLS---TRSNKEDSGRQDDILMEKSPRME 534
 DB 481 IASRPDLS-----HITLPGYVMSNEBQDCLPHSFHEETKEDSGRQDDILMEKSPRME 534

QY 535 SNPDTG 541
 DB 535 SNPDTG 541

RESULT 6

AAB80560

ID AAB80560 standard; Protein; 550 AA.

XX AC

XX AC AAB80560;

XX DT

26-APR-2001 (first entry)

XX DE

Human PTH2 receptor amino acid sequence.

XX KW

Tuberin/fundibular peptide of 39 residues; TIR39; PTH2 receptor ligand;
 parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 antihypertensive; antidiabetic; osteoprotective; hypertensive; cardiac;
 cytotonic; antidiabetic; neuroprotective; PTH receptor antagonist;
 obesity; eating disorder; metabolic disorder; mental disorder;

KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.

OS Homo sapiens.

XX WO200077042-A2.
 XX 21-DEC-2000.

XX 15-JUN-2000; 2000WO-US16776.
 XX 15-JUN-1999; 99US-0139335.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Usdin TB, Hoare SRJ;

XX WPI; 2001-122833/13.
 XX New parathyroid hormone type 2 or 1 receptor ligand, useful for

PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX Example 4; Fig 1; 106pp; English.

XX The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antihypertensive, antidiabetic, osteoprotective,
 CC hypertensive, cardiac, cytostatic, antidiabetic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. The present
 CC sequence represents a PTH2 receptor which is used in the
 CC exemplification of the present invention.

XX SQ Sequence 550 AA;

Query Match 90.3%; Score 2626; DB 22; Length 550;
 Best Local Similarity 91.2%; Pred. No. 3.2e-276;

Matches 499; Conservative 6; Mismatches 30; Indels 12; Gaps 3;

QY 1 MAWLGLSHVWGMLMGLSCLLARALQSDGTTIERQIVLVKAKVQCELNITAIQOE 60

DB 1 MAGLGASLHVWGMLMGLSCLLARALQSDGTTIERQIVLVKAKVQCELNITAIQOE 60

QY 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNK 120

DB 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNK 120

QY 121 NYSDCLRFLOPDISIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTENY 180

DB 121 NYSDCLRFLOPDISIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTENY 180

QY 181 MHLFVSFMLRATSIYFKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQVIGCKIAV 240

DB 181 MHLFVSFMLRATSIYFKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQVIGCKIAV 240

QY 241 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLMGFFILGWGPPAFVAWAARAT 300

DB 241 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLMGFFILGWGPPAFVAWAARAT 300

QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDRKQYRK 360

Db 301 LADARCWELSGDIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDRKQYRK 360
 QY 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSGQFFVSIYCYNGEV 420
 Db 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSGQFFVSIYCYNGEV 420
 QY 421 QAEVKKMSRWNLSDVMKRTPPCGSRRCGSLVTVTHSTSSQSQVAAAHAWCL---SLAK 477
 Db 421 QAEVKKMSRWNLSDVMKRTPPCGSRRCGSLVTVTHSTSSQSQVAAAHAWCL---SLAK 480
 QY 478 LPRSPADSLTATSLYLAWSGTQSRTHSTLS---TRSNKEDSGRQDDILMEKPSRPM 534
 Db 481 IASGRQPS-----HITLPGYVMSNQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 534
 QY 535 SNPDTEG 541
 Db 535 SNPDTEG 541

RESULT 7
 ABU56731
 ID ABU56731 standard; Protein; 561 AA.
 AC ABU56731;

XX 02-APR-2003 (first entry)

XX Lung cancer-associated polypeptide #324.

XX Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX WC20286443-A2.

XX 31-OCT-2002.

XX 18-APR-2002; 2002WO-US12476.

XX 18-APR-2001; 2001US-284770P.

XX 10-MAY-2001; 2001US-290492P.

XX 09-NOV-2001; 2001US-339245P.

XX 13-NOV-2001; 2001US-350666P.

XX 29-NOV-2001; 2001US-334370P.

XX 12-APR-2002; 2002US-372246P.

XX (BOSB-) BOS BIOTECHNOLOGY INC.

XX Aziz N, Murray R;

XX WPI; 2003-093161/08.

XX N-PSDB; ABX76460.

XX Detecting a lung cancer-associated transcript in a cell from a patient

XX for treating lung cancer, by contacting a biological sample from the

XX patient with a polynucleotide that exhibits increased or decreased

XX expression in lung cancer

XX Claim 27; Page 439; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated

XX transcript in a cell from a patient, comprising contacting a biological

XX sample from the patient with a polynucleotide that selectively hybridises

XX to a sequence that is at least 80 % identical to a gene that exhibits

CC cell to treat lung cancer in a patient and for treating a mammal having
 CC lung cancer by administering a modulatory compound identified. The
 CC methods are useful for treating lung cancer, such as small cell lung
 CC cancer, non-small cell lung cancer or other benign or precancerous
 CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
 CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
 CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
 CC and polypeptides are useful for diagnostic purposes and as targets for
 CC screening for therapeutic compounds that modulate lung cancer, such as
 CC antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
 CC polypeptides of the invention.

XX Sequence 561 AA;

Query Match 86.4%; Score 2513; DB 24; Length 561;

Best Local Similarity 91.2%; Pred. No. 6.5e-264;

Matches 477; Conservative 6; Mismatches 28; Indels 12; Gaps 3;

QY 25 QLDSDGTITIERQIVLVKAKVQCELNITAQIQEGEGNCFPEWDGLICWPRGTGKISAV 84

Db 36 QLDSDGTITIERQIVLVKAKVQCELNITAQIQEGEGNCFPEWDGLICWPRGTGKISAV 95

QY 85 PCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTNWYSDCLRFLOPDISIGKQECERL 144

Db 96 PCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTNWYSDCLRFLOPDISIGKQECERL 155

QY 145 YVMYTVGYSISFGSLAVAILIIGYFRRRLHCTRNHYHMHFVSPMLRATSIFFVKDRVVHAH 204

Db 156 YVMYTVGYSISFGSLAVAILIIGYFRRRLHCTRNHYHMHFVSPMLRATSIFFVKDRVVHAH 215

QY 205 IGKHELESIMQDDPONSIEATSVDSQVIGCKIAVVMFYIPLATNYWILVEGLYHNL 264

Db 216 IGKHELESIMQDDPONSIEATSVDSQVIGCKIAVVMFYIPLATNYWILVEGLYHNL 275

QY 265 IFVAFFSDTKYLMGFTLIGNGFPAAFAVAWAVARATLADARCWELSGADIKWIYQAPILA 324

Db 276 IFVAFFSDTKYLMGFTLIGNGFPAAFAVAWAVARATLADARCWELSGADIKWIYQAPILA 335

QY 325 AIGLNFILFNTVRVLATKIWETNAVGHDRKQYRKLAKESTLVLVFVGHYIVFVCLPH 384

Db 336 AIGLNFILFNTVRVLATKIWETNAVGHDRKQYRKLAKESTLVLVFVGHYIVFVCLPH 395

QY 385 SFTGLGWEIRMHCELFNFSGQFFVSIYCYNGEVOAEVKKMSRWNLSDVMKRTPPCG 444

Db 396 SFTGLGWEIRMHCELFNFSGQFFVSIYCYNGEVOAEVKKMSRWNLSDVMKRTPPCG 455

QY 445 SRECGSVLTVTHSTSSQSQVAAAHAWCL---SLAKLPRSPADSLTATSLYLAWSGTQS 501

Db 456 SRECGSVLTVTHSTSSQSQVAAAHAWCL---SLAKLPRSPADSLTATSLYLAWSGTQS 509

QY 502 RTASHTLS---TRSNKEDSGRQDDILMEKPSRPMESNPDTEG 541

Db 510 NSEQDCLPHSFHEETKEDSGRQDDILMEKPSRPMESNPDTEG 552

RESULT 8

AAB80559

ID AAB80559 standard; Protein; 546 AA.

XX AC AAB80559;

XX DT 26-APR-2001 (first entry)

XX XX Rat PTH2 receptor amino acid sequence.

XX Tuberinfundibular peptide of 39 residues; TIR39; PTH2 receptor ligand;

XX parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;

XX PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;

XX antidiabetic; osteoprotective; hypertensive; cardiast;

XX cytotatic; antiasthmatic; neuroprotective; PTH receptor antagonist;

XX obesity; eating disorder; metabolic disorder; mental disorder;

XX depression; schizophrenia; dementia; acute pain; chronic pain; migraine;

XX headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;

Db 1 MGATLIVRTLGLFCGTLSPVGLVDADDVLTKKEQIYLLFNKRCERAIKSKHTSE 60
QY 61 GNCPEWDGLICWPRGTGKISAVCPDPYIDFNHKGVAFRHNCNPNGTWDFMHSLNKTWA 120
Db 61 GSCLPWDGLICWPEGVPGWVSTSCPEYIDFNHKGHAYRCDLNGTWELASHNNKTWA 120
QY 121 NYSDCLRFLOPDISIGKQFCERLYMYVTGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
Db 121 NYSECAKFFPHYNQNERVDFDLRLIYTVGYSISGLSLMVAIVILGYFRRLHCTRYIH 180
QY 181 MHLFVSMRLRATSI FVKDRVVAHIGVKELESIMQDDPQNSTEATSVKSOYIGCKIAV 240
Db 181 MHLFSLMRLRAISIFVKDVLVYSGSALQEMERITV-EDLKSITEAPPANKTQIGCKVAV 239
QY 241 VMFIYELATNYWILVEGLYHNLIFVAFPSDTKYLMGFTLIGWGPFAAFAVAWAVARAT 300
Db 240 TLFYELATNYWILVEGLYHNLIFVAFPSDTKYLMGFTLIGWGPFAAFAVAWAVARAT 299
QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFINTVRVLATKIETNAVGHDTKQYRK 360
Db 300 LATTECDWLSAGNLKWIQIPILTAIVVNFLLFIIRVLATKLRETNAGRCDCRQYRK 359
QY 361 LAKSTLVLVVFGVHYIVFVCLPHS-FTGLGWEIRHCELFNSFQGFVSIYCYCNGE 419
Db 360 LKSTLVLMPLFGVHYIVFVAMPYTESVGLWQIQMHYEMLFNSVQGFVVAIIYCFNGE 419
QY 420 VQAEVKQWNRNLSDVWKRTPPCGSR--RCGSVL--TTVTHSTS 460
Db 420 VQAEIKKANRRRTLALDFKFKARSGNSTYSYGPVMSHTSVTNVTA 464

RESULT 10
AAR90230
ID AAR90230 standard; Protein; 536 AA.
XX AAR90230;
AC AAR90230;
DT 29-AUG-2000 (first entry)
XX Zebrafish PTHr receptor protein sequence.
XX Zebrafish; PTHr receptor; PTH3R receptor; diagnosis; cancer;
KW parathyroid hormone type 1 receptor; parathyroid hormone type 3 receptor.
XX Brachydanio rerio.
XX WO200032771-A1.
XX 08-JUN-2000.
XX 28-MAY-1999; 99WO-US11883.
XX 30-NOV-1998; 98US-0110467.
XX (JUEP/) JUEPPNER H.
XX (RUBI/) RUBIN D A.
XX Jueppner H, Rubin DA;
PI WPI; 2000-412319/35.
XX N-PSDB; AAA30828.
XX Novel zebrafish parathyroid hormone/parathyroid hormone related peptide
PT receptor 3 and isolated nucleic acid encoding zebrafish parathyroid
PT hormone receptor 1 for treating disorders associated with receptor
PT function -
XX Claim 17; Fig 2a; 11lpp; English.
PS This sequence is a parathyroid hormone receptor type 1 (PTH1R)
XX receptor protein of the invention. The invention also relates to a PTH3R
CC receptor protein. Antagonists of PTH1R or PTH3R can be used for the
CC treatment of diseases associated with an increase in PTH1R or PTH3R

CC activity, respectively. The peptides are used for diagnosis or prognosis
CC of diseases and disorders associated with PTH3R or PTH1R, such as cancer.
CC The polypeptides can be used as a molecular weight markers on sodium
CC dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or
CC on molecular sieve gel filtration columns. Antigenic epitope-bearing
CC peptides and polypeptides are useful to raise antibodies, including
CC monoclonal antibodies, that bind specifically to a polypeptide. The
CC peptides are useful during diagnosis of diseases and disorders in
CC mammals involving PTH3R or PTH1R receptor expression or function.
CC Mutations that affect PTH3R or PTH1R sequence and/or expression levels
CC of PTH3R or PTH1R could be diagnostic for patients with disease or
CC disorders of a developmental, physiological or neurological nature. The
CC nucleic acid molecules are valuable for chromosome identification. The
CC mapping of DNAs to chromosomes is an important first step in
CC correlating these sequences with genes associated with disease.
XX
XX Sequence 536 AA;
QY
Query Match 48.8%; Score 1418.5; DB 21; Length 536;
Best Local Similarity 57.8%; Pred. No. 7.9e-145;
Matches 269; Conservative 80; Mismatches 107; Indels 9; Gaps 6;
QY 4 LGASLHV--WGMLMLGSCCL-LARAQDSDGTITIEBQIVLVLKAKVQCELNITAOQEGR 60
Db 1 MGATLIVRTLGLFCGTLSPVGLVDADDVLTKKEQIYLLFNKRCERAIKSKHTSE 60
QY 61 GNCPEWDGLICWPRGTGKISAVCPDPYIDFNHKGVAFRHNCNPNGTWDFMHSLNKTWA 120
Db 61 GSCLPWDGLICWPEGVPGWVSTSCPEYIDFNHKGHAYRCDLNGTWELASHNNKTWA 120
QY 121 NYSDCLRFLOPDISIGKQFCERLYMYVTGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
Db 121 NYSECAKFFPHYNQNERVDFDLRLIYTVGYSISGLSLMVAIVILGYFRRLHCTRYIH 180
QY 181 MHLFVSMRLRATSI FVKDRVVAHIGVKELESIMQDDPQNSTEATSVKSOYIGCKIAV 240
Db 181 MHLFSLMRLRAISIFVKDVLVYSGSALQEMERITV-EDLKSITEAPPANKTQIGCKVAV 239
QY 241 VMFIYELATNYWILVEGLYHNLIFVAFPSDTKYLMGFTLIGWGPFAAFAVAWAVARAT 300
Db 240 TLFYELATNYWILVEGLYHNLIFVAFPSDTKYLMGFTLIGWGPFAAFAVAWAVARAT 299
QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFINTVRVLATKIETNAVGHDTKQYRK 360
Db 300 LATTECDWLSAGNLKWIQIPILTAIVVNFLLFIIRVLATKLRETNAGRCDCRQYRK 359
QY 361 LAKSTLVLVVFGVHYIVFVCLPHS-FTGLGWEIRHCELFNSFQGFVSIYCYCNGE 419
Db 360 LKSTLVLMPLFGVHYIVFVAMPYTESVGLWQIQMHYEMLFNSVQGFVVAIIYCFNGE 419
QY 420 VQAEVKQWNRNLSDVWKRTPPCGSR--RCGSVL--TTVTHSTS 460
Db 420 VQAEIKKANRRRTLALDFKFKARSGNSTYSYGPVMSHTSVTNVTA 464

RESULT 11
AAR92276
ID AAR92276 standard; Protein; 585 AA.
XX AAR92276;
AC AAR92276;
XX 25-MAR-2003 (updated)
DT 18-MAY-1996 (first entry)
XX Opossum kidney PTH/PTHrP receptor.
XX DE
XX Parathyroid hormone; receptor; parathormone; PTH;
KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
KW hypercalcaemia; hypocalcaemia; cancer; opossum.
XX OS
XX Didelphis virginiana.
XX FN
XX US5494806-A.

XX PD 27-FEB-1996.
XX PF 06-APR-1992; 92US-0864475.
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PA (GEO) GEN HOSPITAL CORP.
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI PI Schipani E, Segre GV;
XX DR WPI: 1996-139028/14.
DR N-PSDB; AAT15946.
XX PT DNA encoding vertebrate parathyroid hormone receptor - useful for
PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
PT cancer etc.
XX PS Claim 1; Fig 2A-2E; 64pp; English.
XX CC Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
CC separate genes or of a laboratory artifact. The receptor induces an
CC increase in intracellular cAMP and calcium when challenged with PTH or
CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
CC and hypocalcaemia, to screen for (anti)agonists and to raise antibodies.
CC Host cells expressing the receptor can be used for diagnostic
CC measurement of PTH serum levels.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 585 AA;
Query Match 47.9%; Score 1392; DB 17; Length 585;
Best Local Similarity 47.8%; Pred. No. 6.9e-142;
Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;
QY 24 AQLSDGTTTIEBOIVLVKAKVQCELNITAOQGE----- 60
DB 24 ALVDADDVITKEEQIILLRNAQCEQRLKEVLVPFELAESAKDMWSRS AKTKKPAEK 83
QY 61 -----GNCFPEDWGLICWPRGTGKISAVPCPPYTYDFNHHKVAER 101
DB 84 LYPQAESESVSDRSRLQDGFCLPEWDNIVCWPAGVPGKVAVPCPDYDFNHHKRAYR 143
QY 102 HCNPNGTWDFMHSLNKNTWANSYDCLFLQPDISIGKQECERLYVMYTVGYISFGSLAV 161
DB 144 RCDNSGSMELVPGNNRTWANSYDCLFLQPDISIGKQECERLYVMYTVGYISFGSLAV 201
QY 162 ALLITGYFRRLHCTNRYIHMHFLVSMRLRATSI FVKDRVVHAHIGVKELESIMODDPON 221
DB 202 AVLLIGYFRRLHCTNRYIHMHFLVSMRLRATSI FVKDRVVHAHIGVKELESIMODDPON 260
QY 222 SIATSVDSQVIGCKIAVVMFYFLATNYIMLVNGLYHNLIFVAFPSDKYLMGFLL 281
DB 261 FTEPPPADKAGVGCRCVAVTVFLYFLTTNVMYLVNGLYHNLIFVAFPSDKYLMGFLL 320
QY 282 IGWFFPAAFAVAVAVANILADARCWELSGADIKWYQAPILAAIGNLFILFNTVRVLA 341
DB 321 FGWGLFAVAVAVAVAVANILADARCWELSGADIKWYQAPILAAIGNLFILFNTVRVLA 380
QY 342 TKIETNAVGHTRKOYRKLAISTLVLVNGLYHNLIFVAFPSDKYLMGFLL 400
DB 381 TKLRETNAGCDTRQYRKLLASTLVLVNGLYHNLIFVAFPSDKYLMGFLL 440
QY 401 FNSFQGFVFIICYCNGEVAQVQKWSRWNLSDWKRTPPCGSRRCGSLVLTTHV--- 457
DB 441 FNSFQGFVFIICYCNGEVAQVQKWSRWNLSDWKRTPPCGSRRCGSLVLTTHV--- 493

QY 458 -STSSQVAAAHAWCLSLAKLPRPADSLTATSLYLAWSGYTQSTASTHTLSTRNKED 516
DB 494 VSHTSVTNVGPRGGLALSLS--PRLAPGAGASANGHHQLPGYVYKHGSISEN-SLPSSGPE 550
QY 517 SGRQRDDILM-----EKFSRPMESNPDT 539
DB 551 PGTKDDGYLNGSLYEPVMVGEQPPPLLEERET 583
RESULT 12
AAW73315
ID AAW73315 standard; Protein; 585 AA.
XX AC AAW73315;
XX DT 08-FEB-1999 (first entry)
XX DE Parathyroid hormone receptor OK-O.
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
XX KW PTH-related hypercalcaemia; opossum.
XX OS Didelphis virginiana.
XX PN US5840853-A.
XX PD 24-NOV-1998.
XX PF 06-JUN-1995; 95US-0471494.
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PR 06-JUN-1995; 95US-0471494.
XX PA (GEO) GEN HOSPITAL CORP.
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI PI Schipani E, Segre GV;
XX DR WPI: 1999-034124/03.
DR N-PSDB; AAV08389.
XX PT Antibody to parathyroid hormone receptor - for diagnostic or
PT therapeutic use
XX PS Claim 6; Fig 2; 63pp; English.
XX CC This sequence represents the opossum parathyroid hormone (PTH) receptor
XX OK-O, which is targeted by the antibody of the invention. The antibody
XX of the invention is immunoreactive with naturally occurring human, rat
XX opossum PTH receptor. The antibody is useful for treating disorders
XX characterised by overstimulation of PTH receptors by their ligand and for
XX the diagnosis of PTH-related hypercalcaemia.
XX SQ Sequence 585 AA;
Query Match 47.9%; Score 1392; DB 20; Length 585;
Best Local Similarity 47.8%; Pred. No. 6.9e-142;
Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;
QY 24 AQLSDGTTTIEBOIVLVKAKVQCELNITAOQGE----- 60
DB 24 ALVDADDVITKEEQIILLRNAQCEQRLKEVLVPFELAESAKDMWSRS AKTKKPAEK 83
QY 61 -----GNCFPEDWGLICWPRGTGKISAVPCPPYTYDFNHHKVAER 101
DB 84 LYPQAESESVSDRSRLQDGFCLPEWDNIVCWPAGVPGKVAVPCPDYDFNHHKRAYR 143
QY 102 HCNPNGTWDFMHSLNKNTWANSYDCLFLQPDISIGKQECERLYVMYTVGYISFGSLAV 161
DB 144 RCDNSGSMELVPGNNRTWANSYDCLFLQPDISIGKQECERLYVMYTVGYISFGSLAV 201
QY 162 ALLITGYFRRLHCTNRYIHMHFLVSMRLRATSI FVKDRVVHAHIGVKELESIMODDPON 221

Db 202 AVILIGYFRRLHCTRYIHMHVFSMLRAVSIFIKADVLSGVSTDEIER-ITEBELRA 260
QY 222 STIATSDVSKSYIGCKIAVVMFYFLATNYWILVEGLYLHNIIFVAFFSDTKYLGWIFIL 281
Db 261 FTEPPPADKAGFVGVAVTVFLYLTNYWILVEGLYLHSLIFMAFTSEKKYLGWFTL 320
QY 282 IGVGFPAFVAWAVARATLADARCWELSGADIKWYQAPILAAIGLNFILFNTVRVLA 341
Db 321 FGMLPAFVAVWTVRATLANTECDWDLSSGNKKWIIQVPIILAAIVVNFILFNIIRVLA 380
QY 342 TKIWTNAVGHDTKQYRKLAKTSLVLVLFVGHYIVFVCLPHS-FTGLGWEIRMCSELF 400
Db 381 TKLRETNAGCDTFQYRKLLKSLVLMPLFGVHYIVFMATPYTEVSGILMQVMHYEML 440
QY 401 FNSFQGFVSIYCYCNGEVOAEVKKWSRWNLSDWKRTPPCGSRRCGSVLTTVTH--- 457
Db 441 FNSFQGFVSIYCYCNGEVOAEIKKWSRWTLALDFKKARSGS-----STYSYGP 493
QY 458 -STSSQSOVAAAHAMCLSLAKLPRSPADSLTATSLYLAWSGVTSRTASHTLSTRNKED 516
Db 494 VSHTSVTNVGPGRGLALSLS--PRLAPGAGASANGHHQLPGYVKHGSISEN-SLPSSGPE 550
QY 517 SGRQRDDILM-----EKPSRPMESNPT 539
Db 551 PGTKDDGYLNGSLYEPVMVGEQPPPLLEERET 583
RESULT 13
ID AAR27705
AC AAR27705; Protein; 585 AA.
XX
XX 25-MAR-2003 (updated)
DT 16-MAR-1993 (first entry)
XX
XX Opossum kidney PTH/PTHrP receptor prod. from clone OK-O.
XX Parathyroid hormone; related protein; calcium; antagonist;
KW antibodies; hypercalcaemia.
XX Didelphis virginiana.
XX
XX WO9217602-A1.
XX
XX 15-OCT-1992.
XX
XX 06-APR-1992; 92WO-US02821.
XX
XX 05-APR-1991; 91US-0681702.
PR 06-APR-1992; 92US-0864475.
XX
XX (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
XX
XX Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI Segre GV;
XX
XX N-PSDB; AAQ29605.
DR
DR New DNA encoding parathyroid hormone receptor, DNA and antibodies
PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours
XX
XX Disclosure; Fig 2; 91pp; English.
XX
XX The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
CC receptor protein sequence was deduced from the DNA sequence of the
CC clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O
CC is identical to the OK-H clone except at the C-terminal tail as OK-O
CC encodes a 585 amino acid protein, OK-H encodes one of 515 amino acids.
CC The difference is attributed to a single nucleotide deleted in the OK-H

CC sequence causing a frame shift and an earlier stop codon. It is not
known whether OK-O and OK-H represent prods. of two separate genes or
are a laboratory artifact. The protein may be used in a therapeutic
CC compan. to inhibit activation of PTH or PTHrP and thus reduce the
CC level of calcium in the blood. Cods. capable of competing with PTH
CC or PTHrP for binding can be identified using the protein prod. and
CC DNAs homologous to PTH DNA can be identified using fragments of the
CC clone as probes. The sequence may be used for the prodn. of antibodies
CC useful for the treatment, classification, prognosis and/or treatment of
CC disorders related to the interaction between a cell receptor and a
CC ligand such as in hypercalcaemia. See also AAR27704-16.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 585 AA;
Query Match 47.9%; Score 1391; DB 13; Length 585;
Best Local Similarity 47.8%; Pred. No. 8.9e-142;
Matches 274; Conservative 93; Mismatches 136; Indels 70; Gaps 10;
QY 24 AQLDSGDTTIBEQIVLVLKAKVQCELNT----- 53
Db 24 ALVDADDVITKEEQIILLNAQACEQRLKEVIRVPELAESAKDWMSRSKTKKPAEK 83
QY 54 --AQLQEG-----EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDNHKKVAPR 101
Db 84 LYPQAEESREVSRSRLQDGFCLPEWDNIVCPAGVGVAVVPCPDYDFDNHKKRAVR 143
QY 102 HCNPNGTWDMHSLNKTWANSYDCLRFLOPDISIGKQECERLYVMYTVGYISIFGLAV 161
Db 144 RCDNSGSELVPGNNRTWANSYECVKFLTNETR--EREVFDRLGMIYTVGYISIFGLAV 201
QY 162 ALLIGYFRRLHCTRYIHMHVFSMLRAVSIFIKADVLSGVSTDEIER-ITEBELRA 260
Db 202 AVILIGYFRRLHCTRYIHMHVFSMLRAVSIFIKADVLSGVSTDEIER-ITEBELRA 260
QY 222 STIATSDVSKSYIGCKIAVVMFYFLATNYWILVEGLYLHNIIFVAFFSDTKYLGWIFIL 281
Db 261 FTEPPPADKAGFVGVAVTVFLYLTNYWILVEGLYLHSLIFMAFTSEKKYLGWFTL 320
QY 282 IGVGFPAFVAWAVARATLADARCWELSGADIKWYQAPILAAIGLNFILFNTVRVLA 341
Db 321 FGMLPAFVAVWTVRATLANTECDWDLSSGNKKWIIQVPIILAAIVVNFILFNIIRVLA 380
QY 342 TKIWTNAVGHDTKQYRKLAKTSLVLVLFVGHYIVFVCLPHS-FTGLGWEIRMCSELF 400
Db 381 TKLRETNAGCDTFQYRKLLKSLVLMPLFGVHYIVFMATPYTEVSGILMQVMHYEML 440
QY 401 FNSFQGFVSIYCYCNGEVOAEVKKWSRWNLSDWKRTPPCGSRRCGSVLTTVTH--- 457
Db 441 FNSFQGFVSIYCYCNGEVOAEIKKWSRWTLALDFKKARSGS-----STYSYGP 493
QY 458 -STSSQSOVAAAHAMCLSLAKLPRSPADSLTATSLYLAWSGVTSRTASHTLSTRNKED 516
Db 494 VSHTSVTNVGPGRGLALSLS--PRLAPGAGASANGHHQLPGYVKHGSISEN-SLPSSGPE 550
QY 517 SGRQRDDILM-----EKPSRPMESNPT 539
Db 551 PGTKDDGYLNGSLYEPVMVGEQPPPLLEERET 583
RESULT 14
AAR27275
ID AAR92275 standard; Protein; 515 AA.
XX
XX AAR92275;
AC
XX 25-MAR-2003 (updated)
DT 18-MAY-1996 (first entry)
XX
XX Opossum kidney PTH/PTHrP receptor.
XX Parathyroid hormone; receptor; parathormone; PTH;
KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;

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XX hypercalcaemia; hypocalcaemia; cancer; opossum.
XX OS Didelphis virginiana.
XX PN US5494806-A.
XX PD 27-FEB-1996.
XX PF 06-APR-1992; 92US-0864475.
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PA (GEO ) GEN HOSPITAL CORP.
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX DR WPI; 1996-139028/14.
XX DR N-PSDB; AAT15945.
XX DNA encoding vertebrate parathyroid hormone receptor - useful for
PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
PT cancer etc.
XX PS Claim 1; Fig 1A-1E; 64pp; English.
XX CC Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
CC separate genes or of a laboratory artifact. The receptor induces an
CC increase in intracellular cAMP and calcium when challenged with PTH or
CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
CC Host cells expressing the receptor can be used for diagnostic
CC measurement of PTH serum levels.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 515 AA;

Query Match 47.7%; Score 1388; DB 17; Length 515;
Best Local Similarity 54.6%; Pred. No. 1.5e-141;
Matches 254; Conservative 73; Mismatches 92; Indels 46; Gaps 4;

QY 24 AQLSDGTTTIEEQVLVKAKVQCELNITAOQGE----- 60
Db 24 ALVDADDVTKEEQIILLRNAQAQCEQLKEVLRVPELAESAADMWMSAKTKKPKA 83
QY 61 -----GNCFFPBDGLICWPRTGVGKISAVPCPPYIYDFNHHGVAPR 101
Db 84 LYPQAESREVSRSRLQDGFCLPEWDNIVCWPAGVPGKVAVPCPDYDFNHHGRAVR 143
QY 102 HCNPNGTWDFMHSINKTWANYSDCLRFLOPDISIGQCEFLRYVYTVGYSISGLAV 161
Db 144 RCDNSGSELVPGNNRTWANYSECYKFLTNETR--EREVDFRLGMIYTVGYSISGLSTV 201
QY 162 AILLIGYFRRLHCTRNHYHMLFVSMFLRATSI FVKDRVVHAHIGVKELESIMODDPQN 221
Db 202 AVLLIGYFRRLHCTRNHYHMLFVSMFLRAVSIFIKDAVLVSGVSTDEIER-ITEEELRA 260
QY 222 STEATSVDSKSOYIGKIAVVMFIYLATNYVILVEGLYHNLHIFVAFPSDTKYLWGFTL 281
Db 261 FTEPPPADKAGVGRVATVFLYFLTYNYVILVEGLYHLSLIFWAFSEKKYLWGFTL 320
QY 282 IGWGPAPAFVAAWARATLADARCWELSAGIKWYQAPILAAIGLNFILPLNTVRVLA 341
Db 321 FGWGLFAVFVAWVTVRATLANTECDLSSGNKKWIIQVPIILAAIVNFIINIRVLA 380
QY 342 TKIWETNAVGHDTROKRYKLAESTVLVLVFGVHYIVFVCLPHS-FTGLGWELRMHCELF 400
Db 381 TKLRETNAGRCDTROQYRKLLKSLTLVLMPLFGVHYIVFVMTPTYTRVSGILWQVHYEML 440
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QY 401 FNSFQGFVFSIIYCYCNGEVOAEVVKOMSRWNLSVDNKRTPPCGS 445
Db 441 FNSFQGFVFSIIYCYCNGEVOAEIKKWSRWTLALDFRKARSGS 485
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RESULT 15
AAW73314
ID AAW73314 standard; Protein; 515 AA.
XX AC AAW73314;
XX DT 08-FEB-1999 (first entry)
XX DE Parathyroid hormone receptor OK-H.
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
XX KW PTH-related hypercalcaemia; opossum.
XX OS Didelphis virginiana.
XX PN US5840853-A.
XX PD 24-NOV-1998.
XX PF 06-JUN-1995; 95US-0471494.
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PR 06-JUN-1995; 95US-0471494.
XX PA (GEO ) GEN HOSPITAL CORP.
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX DR WPI; 1999-034124/03.
XX DR N-PSDB; AAV08388.
XX PT Antibody to parathyroid hormone receptor - for diagnostic or
XX PT therapeutic use
XX PS Claim 6; Fig 1; 63pp; English.
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XX CC This sequence represents the opossum parathyroid hormone (PTH) receptor
XX CC OK-H, which is targeted by the antibody of the invention. The antibody
XX CC of the invention is immunoreactive with naturally occurring human, rat or
XX CC opossum PTH receptor. The antibody is useful for treating disorders
XX CC characterised by overstimulation of PTH receptors by their ligand and for
XX CC the diagnosis of PTH-related hypercalcaemia.
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SQ Sequence 515 AA;

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Query Match 47.7%; Score 1388; DB 20; Length 515;
Best Local Similarity 54.6%; Pred. No. 1.5e-141;
Matches 254; Conservative 73; Mismatches 92; Indels 46; Gaps 4;
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QY 24 AQLSDGTTTIEEQVLVKAKVQCELNITAOQGE----- 60
Db 24 ALVDADDVTKEEQIILLRNAQAQCEQLKEVLRVPELAESAADMWMSAKTKKPKA 83
QY 61 -----GNCFFPBDGLICWPRTGVGKISAVPCPPYIYDFNHHGVAPR 101
Db 84 LYPQAESREVSRSRLQDGFCLPEWDNIVCWPAGVPGKVAVPCPDYDFNHHGRAVR 143
QY 102 HCNPNGTWDFMHSINKTWANYSDCLRFLOPDISIGQCEFLRYVYTVGYSISGLAV 161
Db 144 RCDNSGSELVPGNNRTWANYSECYKFLTNETR--EREVDFRLGMIYTVGYSISGLSTV 201
QY 162 AILLIGYFRRLHCTRNHYHMLFVSMFLRATSI FVKDRVVHAHIGVKELESIMODDPQN 221
Db 202 AVLLIGYFRRLHCTRNHYHMLFVSMFLRAVSIFIKDAVLVSGVSTDEIER-ITEEELRA 260
```

QY 222 SIEATSVDKSQYIGCKIAVVMFYFLATNYWILVEGLYLHNLI FVAFFSDTKYLGFTL 281
Db | | :
261 FTEPPADKAGFYGCRVAVTVFLYFLTNTYWILVEGLYLHSLIFMAFFSEKKYLGFTL 320
QY 282 IGMGFPAAFVAAMAVARATLADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRVLA 341
Db | | :
321 FGWGLPAVFVAVVTVRATLANTECDLSSGNKKWIIQVPILAAI VVNFILFINIRVLA 380
QY 342 TKIWTNAVGHDRKQYRKLA KSTLVLVFGVHYIVFVCLPHS-FTGLGWEIRMECELF 400
Db | | :
381 TKLRETNAGRCDRQQYRKLLKSTLVLMPLFGVHYIVFMATPYTEVSGILMQVQMHVEML 440
QY 401 FNSFQGFVSI IYCYCNGEVOAEVKKQMSRWNLSDWKRTPPCGS 445
Db | | :
441 FNSFQGFVVAIIYCFNCGEVQAEIKKSWSRWTLALDFKRXKARSGS 485

Search completed: November 21, 2003, 22:26:02
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: November 21, 2003, 22:25:10 ; Search time 21 Seconds
(without alignments)
1090.008 Million cell updates/sec

Title: US-09-996-569-2
Perfect score: 2907
Sequence: 1 MAWLGLSHVWGMILGSL.....DDILMKPSRPMESNPDTG 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2907	100.0	541	3	US-08-468-011A-2
2	2907	100.0	541	4	US-09-236-468A-2
3	2907	100.0	541	5	PCT-US95-07085-2
4	1672.5	57.5	575	4	US-09-449-632-5
5	1418.5	48.8	536	4	US-09-449-632-2
6	1397	48.1	585	1	US-08-142-439A-6
7	1397	48.1	585	2	US-08-869-477-6
8	1392	47.9	585	2	US-08-142-511B-125
9	1392	47.9	585	2	US-08-468-249A-19
10	1388	47.7	515	2	US-08-468-249A-18
11	1331.5	45.8	591	2	US-08-468-249A-20
12	1331.5	45.8	593	2	US-08-468-249A-21
13	1290.5	44.4	542	4	US-09-449-632-4
14	801	27.6	449	1	US-08-142-439A-5
15	801	27.6	449	2	US-08-869-477-5
16	785	27.0	458	1	US-08-112-817C-2
17	773	26.6	1324	2	US-08-811-897A-56
18	773	26.6	1324	4	US-09-201-474-56
19	713.5	24.5	437	2	US-08-538-816A-2
20	713.5	24.5	437	2	US-09-076-651-2
21	713.5	24.5	437	4	US-09-208-394-2
22	704	24.2	431	2	US-08-538-816A-9
23	704	24.2	431	2	US-09-076-651-9
24	704	24.2	431	4	US-09-208-394-9
25	702.5	24.2	438	2	US-08-538-816A-1
26	702.5	24.2	438	2	US-09-076-651-1
27	702.5	24.2	438	4	US-09-208-394-1

28	696.5	24.0	448	2	US-08-811-897A-18	Sequence 18, Appl
29	696.5	24.0	448	4	US-08-855-213-18	Sequence 18, Appl
30	696.5	24.0	448	4	US-09-201-474-18	Sequence 18, Appl
31	696.5	24.0	467	2	US-08-811-897A-19	Sequence 19, Appl
32	696.5	24.0	467	2	US-08-855-213-19	Sequence 19, Appl
33	696.5	24.0	467	4	US-09-201-474-19	Sequence 19, Appl
34	689.5	23.7	525	2	US-08-811-897A-23	Sequence 23, Appl
35	689.5	23.7	525	2	US-08-855-213-23	Sequence 23, Appl
36	689.5	23.7	525	4	US-09-201-474-23	Sequence 23, Appl
37	688.5	23.7	448	2	US-08-811-897A-16	Sequence 16, Appl
38	688.5	23.7	448	4	US-08-855-213-16	Sequence 16, Appl
39	688.5	23.7	448	4	US-09-201-474-16	Sequence 16, Appl
40	688.5	23.7	485	2	US-08-811-897A-17	Sequence 17, Appl
41	688.5	23.7	485	2	US-08-855-213-17	Sequence 17, Appl
42	688.5	23.7	485	4	US-09-201-474-17	Sequence 17, Appl
43	684.5	23.5	448	2	US-08-811-897A-22	Sequence 22, Appl
44	684.5	23.5	448	2	US-08-855-213-22	Sequence 22, Appl
45	684.5	23.5	448	4	US-09-201-474-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-468-011A-2
; Sequence 2, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-2

Query Match 100.0%; Score 2907; DB 3; Length 541;
Best Local Similarity 100.0%; Pred. No. 9.5e-294;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAWLGLSHVWGMILGSLARQLSDGFTTIEQIVLVKAKVQCELNITQLQEGE 60
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Db 1 MAWLGLSLVWGLMLGSLCLARAQLDSGDTTIEEQIVLVKAKVQCELNITAIQOE 60

QY 61 GNCFFPFDGLICWPGTGVKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNK 120

Db 61 GNCFFPFDGLICWPGTGVKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNK 120

QY 121 NYSCLRLFPDIPISIGKQFCECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRN 180

Db 121 NYSCLRLFPDIPISIGKQFCECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRN 180

QY 181 MHLFVSPMLRATSIYFVKDRVVHAHIGVKELESIMQDDPQNSIEATSDVKSYIGCKIAV 240

Db 181 MHLFVSPMLRATSIYFVKDRVVHAHIGVKELESIMQDDPQNSIEATSDVKSYIGCKIAV 240

QY 241 VMFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAAFVAWAVARAT 300

Db 241 VMFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAAFVAWAVARAT 300

QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLAATKIWETNAVGHDTRKQYRK 360

Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLAATKIWETNAVGHDTRKQYRK 360

QY 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWIRMHCELFNSFGQFFVSIYCYCNGEV 420

Db 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWIRMHCELFNSFGQFFVSIYCYCNGEV 420

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Db 421 QAEVKKMSRWNLSDWKRTPPCGRRCGSVLTTHSTSSOSQVAAAHAWCLSLAKLPR 480

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Db 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKPSRPMESNPOTE 540

QY 541 G 541

Db 541 G 541

RESULT 2

US-09-236-468A-2

Sequence 2, Application US/09236468A

Patent No. 6338951

GENERAL INFORMATION:

APPLICANT: Soppet et al.

TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74

FILE REFERENCE: PF201DI

CURRENT APPLICATION NUMBER: US/09/236,468A

PRIOR FILING DATE: 1999-01-25

PRIOR APPLICATION NUMBER: 08/468,011

PRIOR FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 2

LENGTH: 541

TYPE: PRT

ORGANISM: Homo sapiens

US-09-236-468A-2

Query Match 100.0%; Score 2907; DB 4; Length 541;

Best Local Similarity 100.0%; Pred. No. 9.5e-294;

Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSLVWGLMLGSLCLARAQLDSGDTTIEEQIVLVKAKVQCELNITAIQOE 60

Db 1 MAWLGLSLVWGLMLGSLCLARAQLDSGDTTIEEQIVLVKAKVQCELNITAIQOE 60

QY 61 GNCFFPFDGLICWPGTGVKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNK 120

Db 61 GNCFFPFDGLICWPGTGVKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNK 120

QY 121 NYSCLRLFPDIPISIGKQFCECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRN 180

Db 121 NYSCLRLFPDIPISIGKQFCECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRN 180

QY 181 MHLFVSPMLRATSIYFVKDRVVHAHIGVKELESIMQDDPQNSIEATSDVKSYIGCKIAV 240

Db 181 MHLFVSPMLRATSIYFVKDRVVHAHIGVKELESIMQDDPQNSIEATSDVKSYIGCKIAV 240

QY 241 VMFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAAFVAWAVARAT 300

Db 241 VMFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILGWGFPFAAFVAWAVARAT 300

QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLAATKIWETNAVGHDTRKQYRK 360

Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLAATKIWETNAVGHDTRKQYRK 360

QY 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWIRMHCELFNSFGQFFVSIYCYCNGEV 420

Db 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWIRMHCELFNSFGQFFVSIYCYCNGEV 420

QY 421 QAEVKKMSRWNLSDWKRTPPCGRRCGSVLTTHSTSSOSQVAAAHAWCLSLAKLPR 480

Db 421 QAEVKKMSRWNLSDWKRTPPCGRRCGSVLTTHSTSSOSQVAAAHAWCLSLAKLPR 480

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QY 541 G 541

Db 541 G 541

RESULT 3

PCT-US95-07085-2

Sequence 2, Application PC/TUS9507085

GENERAL INFORMATION:

APPLICANT: Soppet, Daniel R

APPLICANT: Yi, Li

APPLICANT: Rosen, Craig A

APPLICANT: Ruben, Steven

TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor

TITLE OF INVENTION: HLTG74

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,

ADDRESSEE: Stewart & Olstein

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: NJ

COUNTRY: USA

ZIP: 07068-1739

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07085

FILING DATE: 05-JUN-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 325800-393

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 541 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-07085-2

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Query Match 100.0%; Score 2907; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 9.5e-294;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAWLGASHVWGMWMLGSLARQLDSGDTTIEEQIVLVKAKVQCELNITAQLOGE 60
Db 1 MAWLGASHVWGMWMLGSLARQLDSGDTTIEEQIVLVKAKVQCELNITAQLOGE 60
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Db 241 VMFYFLATNYIIVLVEGLYLNLI FVAFPSDTKYLWGFIILIGWGFPAAFVAANAVARAT 300
Qy 301 LADARCWELSGADIKWIYQAPILAAGLNFLNTVRLATKIWETNAVGHDTRKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAGLNFLNTVRLATKIWETNAVGHDTRKQYRK 360
Qy 361 LAKSTLVLVVFGVHYIVFVCLPFSFTGLWEIRMHCELFNSFGQFVSIYCYCNGEV 420
Db 361 LAKSTLVLVVFGVHYIVFVCLPFSFTGLWEIRMHCELFNSFGQFVSIYCYCNGEV 420
Qy 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCLSLAKLPR 480
Db 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCLSLAKLPR 480
Qy 481 SPADSLTATSYLAMSGVTQSRASHTLSRKNKEDSGRQDDILMEKPSRPMESNPDE 540
Db 481 SPADSLTATSYLAMSGVTQSRASHTLSRKNKEDSGRQDDILMEKPSRPMESNPDE 540
Qy 541 G 541
Db 541 G 541

RESULT 4
US-09-449-632-5
; Sequence 5, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: zebrafish
US-09-449-632-5

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Best Local Similarity 60.6%; Pred. No. 3.2e-165;
Matches 321; Conservative 72; Mismatches 110; Indels 27; Gaps 7;

Qy 25 QLSDSGTTIEEQIVLVKAKVQCELNITAQLOEGNCFPEWDLGICWPRGTGKISAV 84
Db 25 QLSDSGTTIEEQIVLVKAKVQCELNITAQLOEGNCFPEWDLGICWPRGTGKISAV 84

Query Match 48.8%; Score 1418.5; DB 4; Length 536;
Best Local Similarity 57.8%; Pred. No. 8e-139;
Matches 269; Conservative 80; Mismatches 107; Indels 9; Gaps 6;

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Qy 61 GNCPEWDLGICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTWA 120
Db 61 GNCPEWDLGICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTWA 120
Qy 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIH 180
Db 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIH 180
Qy 181 MHLFVSFMLRATSI FVKDRVVHAHIGVKELESIMQDDPQNSIEATSVKSYIGCKTAV 240
Db 181 MHLFVSFMLRATSI FVKDRVVHAHIGVKELESIMQDDPQNSIEATSVKSYIGCKTAV 240

Db 56 QAGDEGTEITAEQVQMLLDLAKLQCLQKVSSD--DPAVGVCVPEWDLGICWPGFGTGTXT 114
Qy 85 PCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTWAYSDCLRFLOPDISIGKQFCERL 144
Db 115 PCPPYIYDFNHGAHAYRRCDSSGSSVLAESSNKTWVNYTECIK--SPEPKKRQVFERL 172
Qy 145 YVMTVGYYSISFGSLAVAILIIGYFRRLHCTRNVIHMHLLFVSPMLRATSI FVKDRVVHAH 204
Db 173 HIMYTVGYAVSFSSLLVAIFIIGYFRRLHCTRNVIHMHLLFVSPMLRAASIFVKDRVHTS 232
Qy 205 IGKLESLIMQDDPQNSIEATSVKSYIGCKTAVVMFYFLATNYIIVLVEGLYLNLI 264
Db 233 AGLQESDAVLM--NFTNAVDPVDTSQYMGCKTVLLFIYFLATNYIIVLVEGLYLNLI 291
Qy 265 IFVAFPSDTKYLWGFIILIGWGFPAAFVAANAVARATLADARCWELSGADIKWIYQAPILA 324
Db 292 IFMAFLSDSKYLWGFIILIGWGFPAAFVAANAVARATLADARCWELSGADIKWIYQAPILT 351
Qy 325 AIGLNFLNTVRLATKIWETNAVGHDTRKQYRKLAKESTLVLVVFGVHYIVFVCLPH 384
Db 352 AIGLNFLNTVRLATKIWETNAVGHDTRKQYRKLAKESTLVLVVFGVHYIVFVCLPH 411
Qy 385 SFTGLWEIRMHCELFNSFGQFVSIYCYCNGEVQAEVKKMSRWNLSDVWKRTPPCG 444
Db 412 TFEGLWEIRMHCELFNSFGQFVSIYCYCNGEVQAEVKKMSRWNLSDVWKRTPPCG 471
Qy 445 SRRCGSLVTTVTHSTSSQSOVAAAHAWCLSLAKLPRSPADSLTATSYLAMSGVTQSR 504
Db 472 SNRYGSLVTLGNLSTSSQSLAAGG-----PGTRSTTLFSSRVVRRSGGPTVSHA 522
Qy 505 S---HTLSTRNK-----EDSGRQDDILMEK--PSRPMESNPDE 540
Db 523 TLPGYVLNSDADSLPPSEPEPDSAKQVDDILLKESLPTSPSSGLEDE 572

RESULT 5
US-09-449-632-2
; Sequence 2, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: zebrafish
US-09-449-632-2
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Db 181 MHLFSLRAISIFVKOVLYSGSALOEMERITV-EDLKSITEAPPANKTQFIGCKVAV 239
Qy 241 VMFIYFLATNYWIIWVGLYHNLIFVAFPSDTKLWGLFGFPAFVAAMAVARAT 300
Db 240 TLFLFLATNYWIIWVGLYHNLIFVAFPSDTKLWGLFGFPAFVAAMAVARAT 299
Qy 301 LADARCWELSGADIKWIIQAPILAAIGLNFILNTVRLVATKIWETNAVGHDTKQYRK 360
Db 300 LADTECDLSAGNLKWIQIPILTAIVNLFLLNIIRVLATKLRETNAGRCDDTRQYRK 359
Qy 361 LAKSTLVLVPGVHYIIVFVCLPHS-FTGLGWEIRMHCELPFNSQGFVSIYYCYNGE 419
Db 360 LKSTLVLVPLFGVHYIIVFVCLPHS-FTGLGWEIRMHCELPFNSQGFVSIYYCYNGE 419
Qy 420 VQAEIKKAWNRRTLALDFKRSKARSGSNYYSGPMVSHSIVTNVTA 464
Db 420 VQAEIKKAWNRRTLALDFKRSKARSGSNYYSGPMVSHSIVTNVTA 464

RESULT 6
US-08-142-439A-6
; Sequence 6, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56703600 No. 5670360disk of No. 5670360th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
US-08-142-439A-6

Query Match 48.1%; Score 1397; DB 1; Length 585;
Best Local Similarity 48.0%; Pred. No. 1.6e-136;

Matches 275; Conservative 94; Mismatches 134; Indels 70; Gaps 10;
Qy 24 AQLSDGDTITTEEQILVLKAKVQCELNIT----- 53
Db 24 ALVDADDVITKEEQIILLRNAQAQCEQLKEVLAVPELAESAADMWMSRSAKTKKEKPAEK 83
Qy 54 --AQLQEG-----EGNCFPEWDGLICWPFGTGVGKISAVPCPPYIYDFNKHGVAFR 101
Db 84 LYSQAESREVSRRSLQDGFCLPEWDNIYVCPAGVPGKVVAVPCDFYIYDFNKHGRAYR 143
Qy 102 HCNPNGTWDMHSLNKTWANYSDCLRLFLQPDISIGKQECERLYVMYTVGYISIFSGSLAV 161
Db 144 RCDNSGSMELVFGNNRTWANYSECFLTNETR--EREVFDRLGMIYTVGYISISIGSLTV 201
Qy 162 AILIGIFRRRLHCTRNHYHMLFVSMLEATSIKORVVAHAHIGVKELESIMQDDPON 221
Db 202 AVLILGYFRRRLHCTRNHYHMLFVSMLEATSIKORVVAHAHIGVKELESIMQDDPON 260
Qy 222 SIEATSDVKSYIGCKIAVNMFIYFLATNYWIIWVGLYHNLIFVAFPSDTKLWGLFG 281
Db 261 FTEPPPADKAGFVGCRAVTVFLYFLATTNYWIIWVGLYHNLIFVAFPSDTKLWGLFG 320
Qy 282 IGMGFPAFAVAAVARATLADARCWELSGADIKWIIQAPILAAIGLNFILNTVRLV 341
Db 321 FGWGLPFAVFAVAVTVTRATLANTECNDLSSGNKKWIIQVPIILAAVNVNFIILNIIRVLA 380
Qy 342 TKIWTNAVGHDTKQYRKLAKESTLVLVPGVHYIIVFVCLPHS-FTGLGWEIRMHCELF 400
Db 381 TKLRETNAGRCDDTRQYRKLLKSTLVLVPLFGVHYIIVFVCLPHS-FTGLGWEIRMHCELF 440
Qy 401 FNSQGFVSIYYCYNGEVOAEIKKSWRNLSDVMDHRTPPCGSRRRCGSLVTTVTH--- 457
Db 441 FNSQGFVSIYYCYNGEVOAEIKKSWRNLSDVMDHRTPPCGSRRRCGSLVTTVTH--- 493
Qy 458 -STSSQSOVAHAHAWCLSLAKLPRSPADSLTATSIYLAWSGVTSRTASHTLSRNSKED 516
Db 494 VSHSTVNVNPGRGLALSLS--PRLAPGAGASANGHOLPGVYVXHGSISEN-SLPSSGFE 550
Qy 517 SGRQRDDILM-----EKSPRPMESNPDT 539
Db 551 PGTKDDGYLNGSLGYEPMVGEPPLLEERET 583

RESULT 7
US-08-869-477-6
; Sequence 6, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58467470 No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
; US-08-869-477-6

Query Match 48.1%; Score 1397; DB 2; Length 585;
Best Local Similarity 48.0%; Pred. No. 1.6e-136;
Matches 275; Conservative 94; Mismatches 134; Indels 70; Gaps 10;

QY 24 AQLSDGTTITBEQIVLVKAKVQCELNIT----- 53
Db 24 ALVDADDVITKEBQIILLRNAQACEQLKEVLVPPELAESAADMWRSRSTKKEKPAEK 83
QY 54 --AQLQEG-----EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDNHKGVAFR 101
Db 84 LYSQAESEVSDRSRLQDGFCLPEWDNIWCPAGVPGKVAVPCDFYDFNHHGRAYR 143
QY 102 HCNPGTWDHMSLNKNTWANYSDCLRFIQPDISIGKQFCERLYVMYTVGYISFGSLAV 161
Db 144 RCDNSGSEVSDRSRLQDGFCLPEWDNIWCPAGVPGKVAVPCDFYDFNHHGRAYR 201
QY 162 AILLIGYFRRHLCTRNTHMHLFVSMFLRAVSIFVKDRVVAHIGVKELESIMODDPQN 221
Db 202 AVLLIGYFRRHLCTRNTHMHLFVSMFLRAVSIFIKDAVLYSGVSTDEIER-ITEELRA 260
QY 222 SIATSDVKSOYIGCKIAVVMFIYFLATNYMILVEGLYHLNLIFFVAFFSDTKYLMGFI 281
Db 261 FTEPPPADKAGVGVGRVAVTVFLYTLTNYMILVEGLYHLNLIFFVAFFSEKKYLMGFTL 320
QY 282 LGWGPAAFAVAWAVARATLADARCELSAGDIKNYQAPILAAIQLANFILFLNTRVLA 341
Db 321 FGWGLPAVFAVAVTVTRATLANTECDLSSGNKKWIIQVPIILAAIVVFIPIINIRVLA 380
QY 342 TKIWTNAGHDTRKQYRKLAKSTLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCBELF 400
Db 381 TKLRETNAGCDTRQYRKLAKSTLVLMPLFGVHYIVFMATPYTEVSGILMQVQHYEML 440
QY 401 FNSFGGFVSIYCYCNCEVQAEVKKMSRWMLSDVWKRTPPCGRRRCGSLVTTWTH--- 457
Db 441 FNSFGGFVSIYCYCNCEVQAEIKKMSRWMLTALDFKRKRSQS-----STYSYGM 493
QY 458 -STSSOSVAAAHAAHCLSLAKLPRSPADSLTATSLYLAWSGVQTSRTASHTLSTENKED 516
Db 494 VSHTSVTNVPGRGGLALSLS--PRLAPGAGASANGHQLPGVYKHGSISEN-SLPSGPE 550
QY 517 SGQRDDIIM-----EKSPRPMESNPPT 539
Db 551 PTKDDGYLNGSLYEPWVGEQPPPLLEERT 583

RESULT 8
US-08-142-551B-125
; Sequence 125, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:

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```

; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..585
; OTHER INFORMATION: /note= "PTH receptor"
; US-08-142-551B-125

Query Match 47.9%; Score 1392; DB 2; Length 585;
Best Local Similarity 47.8%; Pred. No. 5.2e-136;
Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;

QY 24 AQLSDGTTITBEQIVLVKAKVQCELNITQLOEGR----- 60
Db 24 ALVDADDVITKEBQIILLRNAQACEQLKEVLVPPELAESAADMWRSRSTKKEKPAEK 83
QY 61 -----GNCFPEWDGLICWPRGTGKISAVPCPPYIYDNHKGVAFR 101
Db 84 LYPQAESEVSDRSRLQDGFCLPEWDNIWCPAGVPGKVAVPCDFYDFNHHGRAYR 143
QY 102 HCNPGTWDHMSLNKNTWANYSDCLRFIQPDISIGKQFCERLYVMYTVGYISFGSLAV 161
Db 144 RCDNSGSEVSDRSRLQDGFCLPEWDNIWCPAGVPGKVAVPCDFYDFNHHGRAYR 201
QY 162 AILLIGYFRRHLCTRNTHMHLFVSMFLRAVSIFVKDRVVAHIGVKELESIMODDPQN 221
Db 202 AVLLIGYFRRHLCTRNTHMHLFVSMFLRAVSIFIKDAVLYSGVSTDEIER-ITEELRA 260
QY 222 SIATSDVKSOYIGCKIAVVMFIYFLATNYMILVEGLYHLNLIFFVAFFSDTKYLMGFI 281
Db 261 FTEPPPADKAGVGVGRVAVTVFLYTLTNYMILVEGLYHLNLIFFVAFFSEKKYLMGFTL 320

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QY 282 ICGGFPAAFAVAWAVARATLADARCHELSAGDIKWIYQAPILAAIGLNFILFINTVRULA 341
Db 321 FCGGLFAVFAVAVVTVRATLANTECWDLSSGNKKWIIQVPIILAAIYVNFILFINIRVLA 380
QY 342 TKIWTNAVGHDRKQYRKLAKTLLVLVFGVHYIVFVCLPHS--FTGLGWEIRHCELF 400
Db 381 TKLRNAGRCDTROQYRKLLKSTLVLMLPLFGVHYIVFVWATPYTEVSGILWQVQHYEML 440
QY 401 FNSFGFFVSIYCYCNGEVOAEVKKWMSRWNLSDVMKRTPPCGSRRCSGLTTVTH--- 457
Db 441 FNSFGFFVSIYCYCNGEVOAEVKKWMSRWNLSDVMKRTPPCGSRRCSGLTTVTH--- 457
QY 458 -STSSQSOVAAAHAWCLSLAKLPRSPADSLTATSLYLAWSGVYQTSHTASHTLSTRNKED 516
Db 494 VSHTSVTVNVPGRGLALSUS--PRLAPGAGASANGHHQLPYGVYKKGSISEN-SLPSSGPE 550
QY 517 SGRQRDDILM-----EKSPRPMESNPD 539
Db 551 PGTCKDGYLNGSLYEPVMEQPPILLEBERET 583

RESULT 9
US-08-468-249A-19
; Sequence 19, Application US/08468249A
; Patent No. 5896148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-19

Query Match 47.9%; Score 1392; DB 2; Length 585;
Best Local Similarity 47.8%; Pred. No. 5.2e-136;
Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;

QY 24 AQLSDGTITIERQIVLVKAKVQCELNITAQIQEGE----- 60
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Db 24 ALVDADDVITKEQIILLNNAQAQCEORLKEVLRVPELAESAQWMSRSKATKKEKPAEK 83
QY 61 -----GNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHNKGAER 101
Db 84 LYPQAEBSREVSRLQDQFCLPEWDNIVCMVAGVPGKVAVPCPDYDFDNHNGRAYR 143
QY 102 HCNPNGTWDFMHSLNKNTWANYSDCLRFLOPDISIGKQECERLYVMYTVGYISIFGSLAV 161
Db 144 RCDSSGSEWELVPGNNRTWANYSECYKFLTNETR--EREVDFRLGMIYTVGYISIGSLTV 201
QY 162 ALIIGYFRRLHCTNYIHMLFVGFMLRATSIYFKVDRVVVHAHIGVKELESIMODDQON 221
Db 202 AVLLIGYFRRLHCTNYIHMLFVGFMLRATSIYFKVDRVVVHAHIGVKELESIMODDQON 260
QY 222 SIEATSVDSQVYIGCKIAYVMFIYFLATNYIYWLVEGLYHLNLIIFVAFPSDTKYLWGFTL 281
Db 261 FTEPPPADKAGFVGCRVAVTVFLYTLTNYIYWLVEGLYHLNLIIFVAFPSDTKYLWGFTL 320
QY 282 ICGGFPAAFAVAWAVARATLADARCHELSAGDIKWIYQAPILAAIGLNFILFINTVRULA 341
Db 321 FCGGLFAVFAVAVVTVRATLANTECWDLSSGNKKWIIQVPIILAAIYVNFILFINIRVLA 380
QY 342 TKIWTNAVGHDRKQYRKLAKTLLVLVFGVHYIVFVCLPHS--FTGLGWEIRHCELF 400
Db 381 TKLRNAGRCDTROQYRKLLKSTLVLMLPLFGVHYIVFVWATPYTEVSGILWQVQHYEML 440
QY 401 FNSFGFFVSIYCYCNGEVOAEVKKWMSRWNLSDVMKRTPPCGSRRCSGLTTVTH--- 457
Db 441 FNSFGFFVSIYCYCNGEVOAEVKKWMSRWNLSDVMKRTPPCGSRRCSGLTTVTH--- 457
QY 458 -STSSQSOVAAAHAWCLSLAKLPRSPADSLTATSLYLAWSGVYQTSHTASHTLSTRNKED 516
Db 494 VSHTSVTVNVPGRGLALSUS--PRLAPGAGASANGHHQLPYGVYKKGSISEN-SLPSSGPE 550
QY 517 SGRQRDDILM-----EKSPRPMESNPD 539
Db 551 PGTCKDGYLNGSLYEPVMEQPPILLEBERET 583

RESULT 10
US-08-468-249A-18
; Sequence 18, Application US/08468249A
; Patent No. 5896148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frasey, Janis K.
; REGISTRATION NUMBER: 34,819
```

```
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-18

Query Match          47.7%; Score 1388; DB 2; Length 515;
Best Local Similarity 54.6%; Pred. No. 1.1e-135;
Matches 254; Conservative 73; Mismatches 92; Indels 46; Gaps 4;

QY 24 AQLSDGRTTIEBQIVLVKAKVOCELNITAOQEGE----- 60
Db 24 ALVDDADDVTKEEQIILLRNAQAQCEQLKEVLRVPELAESAQKDWMSRSAKTKKEKPAEK 83
QY 61 -----GNCFPEWDGLICWPRGTGTVGKISAVPCPPYIYDFNHHGVAFR 101
Db 84 LYPQAESESVSDRSRLQDGFCLPEWDNIVCPAGVPGKVAVPCPDYFYDFNHHGRAYR 143
QY 102 HCNPGTWDPMHSLNKTWANYSDCLREFLOPDISIGKQFCERLYVMYTVGYSGSLAV 161
Db 144 RDSGSMELVPGNNRTWANYSECVKFLNTR--EREVDRGLMITYTVGYSGSLTV 201
QY 162 AILIGYFRRLHCTRNYYHMLFVSMFLRATSFVKDRVVAHIGVKELESIMODDPQN 221
Db 202 AVLLIGYFRRLHCTRNYYHMLFVSMFLRAVSIFIKDAVLYSGVSTDRIER-ITBEELRA 260
QY 222 SIEATSVKSGVIGCKIAVMFYFLATNYXWILVEGLYHNLIFVAFSDTKYLWGFTL 281
Db 261 FTEPPPADKAGVGCVRVAVTVFLYLTNYWILVEGLYHLSLIFWAFPEKKYLWGFTL 320
QY 282 IGMGPAAFAVAWAVARATLADARCWELSGADIKWYQAPILAAIGLNEFILNTRVLA 341
Db 321 FGWGLPFAVFAVAVTVTRATLANTECDLSSGNKKWIIQVPILAAIVNFIINIRVLA 380
QY 342 TKIMETNAVGHTRQYKRLAKSTLVLVFGVHYIVFVCLPHS-FTGLGWIRMEHCELF 400
Db 381 TKLRETNAGRCDTROQYKRLAKSTLVLMPLFVGHVIVFMATYETVSGILWQVQHYEML 440
QY 401 FNSFGQFFVSIYCYCNGEVOAEVKMSRWNLSDWKRTPPCGS 445
Db 441 FNSFGQFFVSIYCYCNGEVOAEIKKSWSRWTLALDFKRSKSGS 485

RESULT 11
US-08-249A-20
; Sequence 20, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-20

Query Match          45.8%; Score 1331.5; DB 2; Length 591;
Best Local Similarity 46.6%; Pred. No. 1.1e-129;
Matches 270; Conservative 86; Mismatches 136; Indels 87; Gaps 11;

QY 22 ARAQLSDGRTTIEBQIVLVKAKVQCE-----LNITAOQEGEGN----- 62
Db 22 AVALVDADDVTKEEQIFLLHRAQAQCKLKEVLHTAANTIMESDKGWTPTASTSGKPRKE 81
QY 63 -----CFPEWDGLICWPRGTGTVGKISAVPCPPYIYDFNHH 96
Db 82 KASGKFYEPSEKENDVPTGSRRRRCPLPEWDNIVCPAGVPGKVAVPCPDYFYDFNHH 141
QY 97 GVAFPHCNPGTWTWPMHSLNKTWANYSDCLREFLOPDISIGKQFCERLYVMYTVGYSGISF 156
Db 142 GHAYRCRDNSEWVPGHNTWANYSECLFMTNTR--EREVDRGLMITYTVGYSGISL 199
QY 157 GSLAVAILIIGYFRRLHCTRNYYHMLFVSMFLRATSFVKDRVVAHIGVKELES- 213
Db 200 ASLTAVAILIAYFRRLHCTRNYYHMLFVSMFLRAASIFVKDAVLYSGFTLDEASRLTEE 259
QY 214 -----IMQDDPQNSTEATSVDSQYIGCKIAVMFYFLATNYXWILVEGLYHNLIFVAF 269
Db 260 ELHIIAQVPPPPAAAAVG-----YAGCRVAVTVFLYLTNYWILVEGLYHLSLIFWAF 314
QY 270 FSDTKYLWGFTLIGWGPAAFAVAWAVARATLADARCWELSGADIKWYQAPILAAIGLN 329
Db 315 FSEKYLWGFTIFGWGLPAVFAVAVTVTRATLANTECDLSSGHKKWIIQVPILASVULN 374
QY 330 FILPLNTVRLATKIWETNAVGHTRQYKRLAKSTLVLVFGVHYIVFVCLPHS-FTG 388
Db 375 FILFINIRVLATKLRETNAGRCDTROQYKRLAKSTLVLVFGVHYIVFVCLPHS-FTG 434
QY 389 LGWEIRMEHCELFNSFGQFFVSIYCYCNGEVOAEVKMSRWNLSDWKRTPPCGSRRC 448
Db 435 TLWQIQHYEMLFNSFGQFFVSIYCYCNGEVOAEIKKSWSRWTLALDFKRSKSGSSY 494
QY 449 GSVLTVTTHSTSSQSVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSG-----VTQS 501
Db 495 --SYGPMVSHTSVTNVGPRAG-----LSLPLSLRPP---ATTNGHSQLPGHAKPGAPATET 546
QY 502 RTASHTLSTRS-----NKEDSGRQDDILMEK 528
Db 547 ETLFVTVMAVPKDDGFLNGSCSLDEEASGSARPPPLQOE 585

RESULT 12
US-08-249A-21
; Sequence 21, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
```



```
RESULT 14
US-08-142-439A-5
; Sequence 5, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56703600 No. 5670360disk of No. 5670360th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
; US-08-142-439A-5
Query Match 27.6%; Score 801; DB 1; Length 449;
Best Local Similarity 37.3%; Pred. No. 1.1e-74;
Matches 176; Conservative 81; Mismatches 149; Indels 66; Gaps 15;

QY 14 LMLGSLARQLDSDGTTIEEQIVLVKAVQCELNITAOI-OEGEGNCPE----- 66
Db 12 LLLRLLLTTKAA-----HTVGVPRLCDVRRVLLERAAHCLQLQSKKKGALGPETASGCE 67
QY 67 --WDGLCWPRGTGKISAVPCPPYIDFNHK-GVAFRHCNPGTWDFMHSLNKTWYNS 123
Db 68 GLWDMNCSWPSAPARTVEVQCPKFLMLSNKNGSLFRNCTODG-----WSE-- 114
QY 124 DCLRFQPDISIG---KQEFCEI-----LYVMVTGVYSFSGSLAVAILIIGVFRILH 173
Db 115 ---TFPRDLACGVNINNSFNERRAYLLKLVMTVGVSSSLMALLVALSILCSFRLIH 171
QY 174 CTRNYHMLFVSMRLATSFVKDVRVHAHGVKVELESIMQDDPQNSIEATSVDKSQY 233
Db 172 CTRNYHMLFVSMRLATSFVKDVRVHAHGVKVELESIMQDDPQNSIEATSVDKSQY 233
; US-08-142-439A-5
Query Match 27.6%; Score 801; DB 2; Length 449;
Best Local Similarity 37.3%; Pred. No. 1.1e-74;
Matches 176; Conservative 81; Mismatches 149; Indels 66; Gaps 15;

QY 234 IGCKIAVVMFIYFLATNYWILVEGLYLNLIFFVAFPSDTKYLWGFILGWGFPAAFAVA 293
Db 213 VGCKLWMIFFQYCIWANYAMLLVEGLYLNLIFFVAFPSDTKYLWGFILGWGSPAFVAL 272
QY 294 WAVARATLADARCWELSA-GDIKWTYQAPILAAIGLNFILFNTVTVLTKIWTNAVGH 352
Db 273 WAITRHFLNTGCMNDINANASVWVIRGPFVILSILNFIFFINILRLMRKLRTQETRGS 332
QY 353 DTRQYRKLAKSTLVLAVFGVHYIVFVCLPHSFTGLGWEIRMHCELPNSFQGFVSII 412
Db 333 ET-NHYKKLAKSTLILFIIFGHIYIVFAFSPED----AMEVQLFFELALGSEQGLVAVL 387
QY 413 YCYCNGEYQAEYKXKMSRWNLSDVMKTRTPPGCRRRCGSLVLTVTHTSTSSQSO 464
Db 388 YCFLNGEVQLEVQKKRWQHLQ-EPLRPVAFNNSFNATNGPTHSTKASTE 438

RESULT 15
US-08-869-477-5
; Sequence 5, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
; US-08-869-477-5
Query Match 27.6%; Score 801; DB 2; Length 449;
Best Local Similarity 37.3%; Pred. No. 1.1e-74;
Matches 176; Conservative 81; Mismatches 149; Indels 66; Gaps 15;
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Matches 176; Conservative 81; Mismatches 149; Indels 66; Gaps 15;
QY 14 LMLGSCILARAQLSDGTTIEBQIVLVKAKVQCELNITAOI-QBEGNCFPE----- 66
Db 12 LLRLRLLLTKAA---HTGVPPRLCDVRRVLLEERAHCIQQLSKEKGALGPETASGCE 67
QY 67 --WDGLICWPRGTGVIKISAVPCPPYIYDENHK-GVAFRHCNPNGTWDPMHSLNKTWANY 123
Db 68 GLMDNMSCWPSSAPARTIVEQCFLMLMUSNKNKGSIFRNCTQDG-----WSE-- 114
QY 124 DCLRFIQPDISIG---KQBFCEP-----LYVMYTVGYISFGSLAVAILIIGYFRLH 173
Db 115 ---TFRPDLAGCVNNNSFNERRHAYLLKLVMYTVGYSSSLAMLLVALSILCSFRLH 171
QY 174 CTRNYIHMHLFVSGFMLRATSI FVKDRVYHAHIGVKELESIMODDPQNSIEATSVDKSQY 233
Db 172 CTRNYIHMHLFVSFILRALSNFIKDAV-----LFSSDD-----VTYCD-AHK 212
QY 234 IGGKIAVVMFIYFLATNYVYLVEGLYLNHLIFVAFPSDTKYLWGFILIGWGPAAAFVAA 293
Db 213 VGCKLVNIFFOYCIMANYAWLLVEGLYLNHLIFVAFPSDTKYLWGFILIGWGPAAAFVAA 272
QY 294 WAVARATLADARCWELSA-GDIKWIYCAPILAAIGLNFIPLNTVRVLTAKIWTNAUGH 352
Db 273 WAITRHELENTGCDINANASVWVIRGVPVILSILINFIFFINILRLMKLRTQETRGS 332
QY 353 DTRKQYRKLAKTSLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFGPFVSII 412
Db 333 ET-NHYKRLAKSTLLIPLFGIHYIVFAFSPED---AMEVQLFFELALGSFQGLVVAVL 387
QY 413 YCYCNGEVOAEVKKMSRNLSVDWKRTPPCGSRRCGSLTIVTTHSTSSQSQ 464
Db 388 YCFLNGEVOLEVOKKRWQHLQ-EFPLRPVAFNNSFNATNGTHTSTKASTE 438
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Search completed: November 21, 2003, 22:28:30
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 22:27:30 ; Search time 35 Seconds

(without alignments)
2821.848 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 2907

Sequence: 1 MAWLGAHLVWGMMLGSL.....DDILMEKPSRPWESNPDTREG 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2635	90.6	550	15	US-10-225-567A-227
2	2629	90.4	550	12	US-09-826-509-565
3	2600	89.4	550	15	US-10-014-162-110
4	2213.5	76.1	546	15	US-10-014-162-109
5	1672.5	57.5	575	12	US-10-372-095-5
6	1418.5	48.8	536	12	US-10-372-095-2
7	1392	47.9	585	12	US-10-267-730-19
8	1388	47.7	515	12	US-10-267-730-18
9	1345.5	46.3	595	10	US-09-943-446-6
10	1336.5	46.0	593	10	US-09-943-446-9
11	1336.5	46.0	593	15	US-10-225-567A-229
12	1331.5	45.8	591	10	US-09-943-446-7
13	1331.5	45.8	591	12	US-10-267-730-20
14	1331.5	45.8	593	12	US-10-267-730-21
15	1330.5	45.8	593	12	US-09-826-509-563

16	1324	45.5	591	10	US-09-943-446-8	Sequence 8, Appli
17	1290.5	44.4	542	12	US-10-372-095-4	Sequence 4, Appli
18	962.5	33.1	964	12	US-10-017-161-710	Sequence 710, App
19	784	27.0	440	15	US-10-225-567A-310	Sequence 310, App
20	778	26.8	440	12	US-09-826-509-567	Sequence 567, App
21	773	26.6	1324	10	US-09-935-371-56	Sequence 56, Appli
22	759.5	26.1	457	15	US-10-225-567A-469	Sequence 469, App
23	753.5	25.9	457	12	US-09-826-509-579	Sequence 579, App
24	702.5	24.2	438	15	US-10-157-031-237	Sequence 237, App
25	702.5	24.2	438	15	US-10-225-567A-471	Sequence 471, App
26	702	24.1	438	11	US-09-983-000A-20	Sequence 20, Appli
27	696.5	24.0	438	12	US-09-826-509-581	Sequence 581, App
28	696.5	24.0	448	10	US-09-935-371-18	Sequence 18, Appli
29	696.5	24.0	467	10	US-09-935-371-19	Sequence 19, Appli
30	689.5	23.7	525	10	US-09-935-371-23	Sequence 23, Appli
31	689.5	23.7	525	14	US-10-044-722-3	Sequence 3, Appli
32	689.5	23.7	525	15	US-10-225-567A-231	Sequence 231, App
33	688.5	23.7	448	10	US-09-935-371-16	Sequence 16, Appli
34	688.5	23.7	485	10	US-09-935-371-17	Sequence 17, Appli
35	684.5	23.5	448	10	US-09-935-371-22	Sequence 22, Appli
36	681.5	23.4	476	10	US-09-935-371-20	Sequence 20, Appli
37	681.5	23.4	495	10	US-09-935-371-21	Sequence 21, Appli
38	679	23.4	468	12	US-09-826-509-553	Sequence 553, App
39	675	23.2	552	10	US-09-935-371-27	Sequence 27, Appli
40	674.5	23.2	553	10	US-09-935-371-25	Sequence 25, Appli
41	673.5	23.2	476	10	US-09-935-371-14	Sequence 14, Appli
42	673.5	23.2	513	10	US-09-935-371-15	Sequence 15, Appli
43	672.5	23.1	553	10	US-09-935-371-29	Sequence 29, Appli
44	670	23.0	475	10	US-09-935-371-26	Sequence 26, Appli
45	669.5	23.0	476	10	US-09-935-371-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1

US-10-225-567A-227
; Sequence 227, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225.567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-227

Query Match 90.6%; Score 2635; DB 15; Length 550;
Best Local Similarity 91.4%; Pred. No. 1.3e-251;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

QY 1 MAWLGAHLVWGMMLGSLARQLSDGTITIEEQIVLVKAKVCELNITAQLOGE 60
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Db 1 MAWLGAHLVWGMMLGSLARQLSDGTITIEEQIVLVKAKVCELNITAQLOGE 60

QY 61 GNCPEPDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFFHCNPNGTWDFMHSINKTWA 120
|||
Db 61 GNCPEPDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFFHCNPNGTWDFMHSINKTWA 120

QY 121 NYSCLRFLOPDISIGKQEFERLYVMYTVGVSYISFGSLAVAILIIGYFRRLHCTRNVIH 180
|||
Db 121 NYSCLRFLOPDISIGKQEFERLYVMYTVGVSYISFGSLAVAILIIGYFRRLHCTRNVIH 180


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QY 181 MHLFVSFMLRATSI FVKDRVVVHAHIGVKELESIMQDDPQNSIEATSVDSQYIGCKIAV 240
|||
Db 181 MHLFVSFMLRATSI FVKDRVVVHAHIGVKELESIMQDDPQNSIEATSVDSQYIGCKIAV 240
|||
QY 241 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLWGFFILIGWGPFAAFVAWAVARAT 300
|||
Db 241 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLWGFFILIGWGPFAAFVAWAVARAT 300
|||
QY 301 LADARCWELSGAGDIKWIYQAPILAAI GLNFILFLNTVRVLATKIWETNAVGHDTKQYRK 360
|||
Db 301 LADARCWELSGAGDIKWIYQAPILAAI GLNFILFLNTVRVLATKIWETNAVGHDTKQYRK 360
|||
QY 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIYCYCNGEV 420
|||
Db 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIYCYCNGEV 420
|||
QY 421 QAEVKKMSRWNLSDVWKRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
|||
Db 421 QAEVKKMSRWNLSDVWKRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
|||
QY 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
|||
Db 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
|||
QY 535 SNPDTEG 541
|||
Db 535 SNPDTEG 541
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RESULT 2
US-09-826-509-565
; Sequence 565, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 565
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-565

Query Match 90.4%; Score 2629; DB 12; Length 550;
Best Local Similarity 91.2%; Pred. No. 4.9e-251;
Matches 499; Conservative 6; Mismatches 30; Indels 12; Gaps 3;

QY 1 MAWLGASLHVWGLMLGSCLLARAQLDSGTTTIEEQIVLVKAKVQCELNITAOQEGE 60
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Db 1 MAGLGASLHVWGLMLGSCLLARAQLDSGTTTIEEQIVLVKAKVQCELNITAOQEGE 60
|||
QY 61 GNCFFEWGDLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWA 120
|||
Db 61 GNCFFEWGDLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWA 120
|||
QY 121 NYSDCLEFLQPDISIGKQEFCEFLRYVMYTVGVYSISFGSLAVAILIIGYFRRHLCTRNVIH 180
|||
Db 121 NYSDCLEFLQPDISIGKQEFCEFLRYVMYTVGVYSISFGSLAVAILIIGYFRRHLCTRNVIH 180
|||
QY 181 MHLFVSFMLRATSI FVKDRVVVHAHIGVKELESIMQDDPQNSIEATSVDSQYIGCKIAV 240
|||
Db 181 MHLFVSFMLRATSI FVKDRVVVHAHIGVKELESIMQDDPQNSIEATSVDSQYIGCKIAV 240
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Db 181 MHLFVSFMLRATSI FVKDRVVVHAHIGVKELESIMQDDPQNSIEATSVDSQYIGCKIAV 240
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QY 241 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLWGFFILIGWGPFAAFVAWAVARAT 300
|||
Db 241 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLWGFFILIGWGPFAAFVAWAVARAT 300
|||
QY 301 LADARCWELSGAGDIKWIYQAPILAAI GLNFILFLNTVRVLATKIWETNAVGHDTKQYRK 360
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Db 301 LADARCWELSGAGDIKWIYQAPILAAI GLNFILFLNTVRVLATKIWETNAVGHDTKQYRK 360
|||
QY 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIYCYCNGEV 420
|||
Db 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIYCYCNGEV 420
|||
QY 421 QAEVKKMSRWNLSDVWKRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
|||
Db 421 QAEVKKMSRWNLSDVWKRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
|||
QY 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
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Db 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
|||
QY 535 SNPDTEG 541
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Db 535 SNPDTEG 541
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RESULT 3
US-10-014-162-110
; Sequence 110, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-162-110

Query Match 89.4%; Score 2600; DB 15; Length 550;
Best Local Similarity 90.9%; Pred. No. 3.6e-248;
Matches 498; Conservative 6; Mismatches 30; Indels 14; Gaps 5;

QY 1 MAWLGASLHVWGLMLGSCLLARAQLDSGTTTIEEQIVLVKAKVQCELNITAOQEGE 60
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Db 1 MAGLGASLHVWGLMLGSCLLARAQLDSGTTTIEEQIVLVKAKVQCELNITAOQEGE 60
|||
QY 61 GNCFFEWGDLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWA 120
|||
Db 61 GNCFFEWGDLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWA 120
|||
QY 121 NYSDCLEFLQPDISIGKQEFCEFLRYVMYTVGVYSISFGSLAVAILIIGYFRRHLCTRNVIH 180
|||
Db 121 NYSDCLEFLQPDISIGKQEFCEFLRYVMYTVGVYSISFGSLAVAILIIGYFRRHLCTRNVIH 180
|||
QY 181 MHLFVSFMLRATSI FVKDRVVVHAHIGVKELE-SLIMQDDPQNSIEATSVDSQYIGCKIA 239
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Db 181 MHLFVSFMLRATSI FVKDRVVVHAHIGVKELESLIMQDDPQNSIEATSVDSQYIGCKIA 240
|||
QY 240 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLWGFFILIGWGPFAAFVAWAVARA 299
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Db 240 VMFIYFLATNYWILVEGLYLNHLIFVAFSDTKYLWGFFILIGWGPFAAFVAWAVARA 299
|||
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Qy 300 TLADARCWELSGADIKWIIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDTKQYR 359
Db 300 TLADARCWELSGADIKWIIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDTKQYR 359
Qy 360 KLAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELPFNSFQGFVSIYCYCNGE 419
Db 360 KLAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELPFNSFQGFVSIYCYCNGE 419
Qy 420 VQAEVKWMSRWNLSDVMKRTPPCGSRRCGSLVTTVTHSTSSQQAHAHAWCL---SLA 476
Db 420 VQAEVKWMSRWNLSDVMKRTPPCGSRRCGSLVTTVTHSTSSQQAHAHAWCL---SLA 476
Qy 477 KLPSPADSLTATSIYLAWSGVTSRTASHTLS---TFSNKEDSGRQDDILMEKPSRPM 533
Db 480 KIARQPDSD-----HITLPGYVNSNQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 533
Qy 534 ESNPDTEG 541
Db 534 ESNPDTEG 541
RESULT 4
US-10-014-162-109
; Sequence 109, Application US/10014162
; Publication No. US2003032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(546)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-014-162-109

Query Match 76.1%; Score 2213.5; DB 15; Length 546;
Best Local Similarity 76.5%; Pred. No. 6.2e-210;
Matches 416; Conservative 37; Mismatches 82; Indels 9; Gaps 4;
Qy 1 MAWLGAISHVGMGLGSLARALQSDGTTITIEEQIVLVKAKVOCELNITAQLOEGE 60
Db 1 MPWLEALPYICGMILRLSLVGLQSLDGGTTITIEEQIVLVKAKVOCELNITAQLOEGE 60
Qy 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSINKTWA 120
Db 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSINKTWA 120
Qy 121 NYSCLRLPDDISIGKQEFCEYVVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
Db 121 NYSCLRLPDDISIGKQEFCEYVVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
Qy 181 MHLFVSMRLRATSIYFVDRVVAHIGVKELESIMQDDPQNSIATSVDSKQYIGCKIAV 240
Db 179 LHLFVSMRLRATSIYFVDRVVAHIGVKELESIMQDDPQNSIATSVDSKQYIGCKIAV 238
Qy 241 VMFYIYFATNYYWILVEGLYLHNLIYVAFPSDITKYLWGFILIGWGFPAAFVAAWAVARAT 300
Db 239 VMFYIYFATNYYWILVEGLYLHNLIYVAFPSDITKYLWGFILIGWGFPAAFVAAWAVARAT 298

Qy 301 LADARCWELSGADIKWIIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDTKQYR 360
Db 299 LADARCWELSGADIKWIIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDTKQYR 357
Qy 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELPFNSFQGFVSIYCYCNGE 420
Db 358 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELPFNSFQGFVSIYCYCNGE 417
Qy 421 QAEVKWMSRWNLSDVMKRTPPCGSRRCGSLVTTVTHSTSSQQAHAHAWCLSLAKLPR 480
Db 418 QAEVKWMSRWNLSDVMKRTPPCGSRRCGSLVTTVTHSTSSQQAHAHAWCLSLAKLPR 477
Qy 481 SPA---DSLTSATSIYLAWSGVTSRTASHTLS---TFSNKEDSGRQDDILMEKPSRPM 537
Db 478 TACQIDSHVTLPGYVNSNQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 534
Qy 538 DTEG 541
Db 535 DTEG 538
RESULT 5
US-10-372-095-5
; Sequence 5, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: PTHR AND PTHR Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-5
Query Match 57.5%; Score 1672.5; DB 12; Length 575;
Best Local Similarity 60.6%; Pred. No. 2.2e-156;
Matches 321; Conservative 72; Mismatches 110; Indels 27; Gaps 7;
Qy 25 QLSDGHTITIEEQIVLVKAKVOCELNITAQLOEGENCPFNDGLICWPRGTGKISAV 84
Db 56 QAGEDGHTITIEEQIVLVKAKVOCELNITAQLOEGENCPFNDGLICWPRGTGKISAV 114
Qy 85 PCPEYIYDFNKHGVAFRHCNPNGTWDFMHSINKTWAISDCLRLPDDISIGKQEFCEY 144
Db 115 PCPEYIYDFNKHGVAFRHCNPNGTWDFMHSINKTWAISDCLRLPDDISIGKQEFCEY 172
Qy 145 VMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTHYFVDRVVAHIGVKELESIMQDD 204
Db 173 HMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTHYFVDRVVAHIGVKELESIMQDD 232
Qy 205 IGKLESLIMQDDPQNSIATSVDSKQYIGCKIAVVMFYIYFATNYYWILVEGLYLHN 264
Db 233 AGLQESDAVLM--NNFTAVDPAVDTSOYMGCKVTLVLFYFATNYYWILVEGLYLHN 291
Qy 265 IFVAFPSDITKYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSGADIKWIIYQAP 324
Db 292 IFVAFPSDITKYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSGADIKWIIYQAP 351
Qy 325 AIGLNFILNTVRLATKIWETNAVGHDTKQYRKLAKSTLVLVVFGVHYIVFVCLPH 384
Db 352 AIGLNFILNTVRLATKIWETNAVGHDTKQYRKLAKSTLVLVVFGVHYIVFVCLPH 411
Qy 385 SFTGLGWEIRMHCELPFNSFQGFVSIYCYCNGEQAEBVKWMSRWNLSDVMKRTPPCG 444

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Db 412 TPEGWBERMYCELFNFQGFVSIYCYNGEVQTEIKKTTWTRNNLAFQWGPVVG 471
Qy 445 SRRCGSLVTTVTHSTSSQVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSR 504
Db 472 SNRYGSLVTLGNSSSSQSLAAG-----FCSTRSTLFPSSRYSSGGPTVSTHA 522
Qy 505 S---HTLSTRNK-----EDGRQRDDILMEK--PSRPMESNPOTE 540
Db 523 TLPGVVNSDADSLPSPIDEEPEDSAKQVDDILLKESLTPRSPSGLEDDE 572

RESULT 6
US-10-372-095-2
; Sequence 2, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-2

Query Match 48.8%; Score 1418.5; DB 12; Length 536;
Best Local Similarity 57.8%; Pred. No. 2.6e-131;
Matches 269; Conservative 80; Mismatches 107; Indels 9; Gaps 6;

Qy 4 LGASLHV--WGWLMLGSCI--LARAQLDSGTTTIEQIVLVKAKVOCELNITAOQGE 60
Db 1 MGATLIVTLGLFCGTLSSFYVGLVDADDVLTKQEQIYLLFNARKERAIKSKHKTSE 60
Qy 61 GNCPEWDGLICWPRTGTVGKISAVCPPIYDFNKHGVAFCNPNGTWDFMHSLNKTTWA 120
Db 61 GSCLEWDGILCWPEGVGPKVMTSCPEYIYDFNKHGHAYRCDLNGTWELASHNNKTWA 120
Qy 121 NYSDCRLRFLQDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRHLHCTRNTH 180
Db 121 NYSECAKFFPHYNQOEREVDFRLYIYTVGYSISGLSLMVAIVTLGYFRRHLHCTRNTH 180
Qy 181 MHLFVSFMLRATSIYFKDVRVVAHIGVKELESIMQDDPPQNSIEATSDKQYIGCKIAV 240
Db 181 MHLFSLFMLRAISIFVKDVLVSGSALQEMERITV-EDLKSITEAPPANKTQFICKYAV 239
Qy 241 VMFIYFLATNYIWLVEGLYHLNLFVAFSTKYLWGFILGWGPPAAPVAAWAVARAT 300
Db 240 TLFYFLATNYIWLVEGLYHLSLFTMFPFSDRKYLWGFILGWGVPAMFVTIWSVRAT 299
Qy 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFINTVRLATKIWETNAVGHDTKQYRK 360
Db 300 LADTECWDLSAGNLKWIYQIPLITAIIVNFFLFIIRVLATPKLRETNAGRCTDQYRK 359
Qy 361 LAKSTLVLVFGVHYIVFVCLPHS--FTGLGWEIRMHCELFNSFGPFVSIYCYNGE 419
Db 360 LKSTLVLMPLFGVHYIVFPMAMPYTEVSGVLWQIQWHEMLEFNSVQGFVAILIYCFNGE 419
Qy 420 VQAEVKKMSRWNLSDVWKRTPPCGSR--RCGSVL--TTVTHSTS 460
Db 420 VQAEIKKAWNRRTALDPFKRKARSGSNTSYSGPVMVSHTSVNTVTA 464
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RESULT 7

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US-10-267-730-19
; Sequence 19, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARACHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-19

Query Match 47.9%; Score 1392; DB 12; Length 585;
Best Local Similarity 47.8%; Pred. No. 1.3e-128;
Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;

Qy 24 AQLSDSGTITIERQIVLVKAKVOCELNITAOQGE----- 60
Db 24 ALVDADDVITKEEQIILLRNAQAOCEORLKVLRVPLEAESAADMWMSAKTKKEKPAEK 83
Qy 61 -----GNCPEWDGLICWPRTGTVGKISAVCPPIYDFNKHGVAFR 101
Db 84 LYPQAESESVSDRSRLQDGFCLPEWDNIVCWPGVPGKVAVPCDFYDFNKHGGRAYR 143
Qy 102 HCNPNGTWDFMHSLNKWTWANYSDCLRFLQDISIGKQFCERLYVMYTVGYSISFGSLAV 161
Db 144 RCDSSGMELVGNNRTWANYSECYKFLTNETR--EREVDFRLGMIYTVGYSISGLSLTV 201
Qy 162 ALLIIGYFRRHLHCTRNTHMHLFVSFMLRATSIYFKDVRVVAHIGVKELESIMQDDPQN 221
Db 202 AVLILGYFRRHLHCTRNTHMHLFVSFMLRATSIYFKDVRVVAHIGVKELESIMQDDPQN 260
Qy 222 SIETATSDKQYIGCKIAVVMFIYFLATNYIWLVEGLYHLNLFVAFSTKYLWGFIL 281
Db 261 FTEPPADKAGVGVCAVTVFLYFLITNYIWLVEGLYHLSLFPMAFSEKKYLWGFIL 320
Qy 282 IGWGFPAAFVAAWAVARATLADARCWELSGADIKWIYQAPILAAIGLNFILFINTVRLA 341
Db 321 FGWGLPAVFVAWVTVTRATLANTECWDLSGNGKMWIIQVPIAAIIVNFILFINIIRVLA 380
Qy 342 TKIWETNAVGHDTKQYRKSLAKSTLVLVFGVHYIVFVCLPHS--FTGLGWEIRMHCELF 400
Db 381 TKLRETNAGRCTDQYRKLLKSTLVLMPLFGVHYIVFPMATPYTEVSGILWQVQMHYEML 440
Qy 401 FNSFGPFVSIYCYNGEVOAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTH--- 457
Db 441 FNSQGFVAILIYCFNGEVOAEIKKSWRWTALDFRKARSGS-----STVSYGPM 493
Qy 458 -STSSQSOVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSRSTASHTLSRKNED 516
Db 494 VSHTSVTVNGVPRGGLALSLS--PRLAPGAGASANGHQLPGVVKHGSISEN-SLPSSGPE 550
Qy 517 SGQRQDDILM-----EKSPRPMESNPDT 539
Db 551 PGTKDDGYLNGSLGYPEVMVGEQPPPLLEERET 583

RESULT 8
US-10-267-730-18
; Sequence 18, Application US/10267730
; Publication No. US20030153041A1
```

GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-18

Query Match 47.7%; Score 1388; DB 12; Length 515;
Best Local Similarity 54.6%; Pred. No. 2.6e-128;
Matches 254; Conservative 73; Mismatches 92; Indels 46; Gaps 4;

QY 24 AQLDSGDTITIEQIVLVKAKVQCELNITAOLOSGE----- 60
Db 24 ALVDADDVITKEEQIILLNNAQCEQRKEVIRVPELAESAKOWMSRSATKYEKPAEK 83

QY 61 -----GNCFPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFR 101
Db 84 LYPQAESESVSDRSELQDGFCLPENDINGVCPAGVPGKVAVPCPDYIDFNHKGRAVR 143

QY 102 HCNPNGTWDFMHSLNKNTWANYSDCLRFLQPDISIGKQECERLYVMYTVGYSISFGSLAV 161
Db 144 RCDNSGSELVPGNNRTWANYSECVKFLTNETR--EREVDFRLGMIYTVGYSISGLSTV 201

QY 162 ALLIGYFRRHLCTNYTHMHLFVSEFMRATSIKVKDRVVAHAHIGVKELESIMODDPQN 221
Db 202 AVLLIGYFRRHLCTNYTHMHLFVSEFMRATSIKVKDRVVAHAHIGVKELESIMODDPQN 260

QY 222 STEATSVDKSOYIGCKIAVVMFIYFLATNYVILVEGLYHLNLIIFVAPFSDTKYLGWFTL 281
Db 261 FTEPPADKAGVGRVAVTVFLYFLTNYVILVEGLYHLNLIIFVAPFSEKKYLGWFTL 320

QY 282 IGWGPAAFAVAWAVARATLADARCELSAGDIKTIYQAPILAAIGLNFILFLNTVRVLA 341
Db 321 FCGGLPAFVAVAVTVATLANTECWDLSGNGKWIIOVPILAAIWNFILFINIIRVLA 380

QY 342 TKIMETNAVGHDTKQYRKLAKSTLVLVLFVGHVHIVFVCLPHS--FTGLGWEIFRMHCLIF 400
Db 381 TKLRETNAGRCDTQOYRKLAKSTLVLVLFVGHVHIVFVCLPHS--FTGLGWEIFRMHCLIF 440

QY 401 FNSFGQFFVYIYFCNGEVOAEVKKWSRNLSVDKRTTPCGS 445
Db 441 FNSFGQFFVYIYFCNGEVOAEVKKWSRNLSVDKRTTPCGS 485

RESULT 9
US-09-943-446-6
; Sequence 6, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PCI0891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170

GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-18

Query Match 46.3%; Score 1345.5; DB 10; Length 595;
Best Local Similarity 46.5%; Pred. No. 5.1e-124;
Matches 281; Conservative 90; Mismatches 154; Indels 79; Gaps 11;

QY 4 LGASLHVWGLMLGSCLL--ARAQLOSDGDTITIEQIVLVKAKVQCELNITAOLO--- 57
Db 1 MGAURIAPGLALLLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCKRLKVLQORPA 60

QY 58 -----EGEGN-----CFPEWDGLICWPR 75
Db 61 DIMESDKGASASTSGKPKKEKASGKLYPESEDEKVEPTGSRHGRPCLPENDHILCWPL 120

QY 76 GTVGKISAVPCPPYIDFNHKGVAFRHCHNPNGTWDFMHSLNKNTWANYSDCLRFLQPDISI 135
Db 121 GAPGEVAVPCPDYIDFNHKGVAFRHCHNPNGTWDFMHSLNKNTWANYSDCLRFLQPDISI 179

QY 136 GKQECERLYVMYTVGYSISFGSLAVALLIGYFRRHLCTNYTHMHLFVSEFMRATSIK 195
Db 180 -EREVDFRLGMIYTVGYSISGLSTVAVLLIAYFRRHLCTNYTHMHLFVSEFMRATSIK 238

QY 196 VKDRVVAHAHIGVKELESIMODDPQNSTEATSVDKSOYIGCKIAVVMFIYFLA 248
Db 239 VKDAVLYSGATLDEAERLTSEELRAIAQAPPPPTAAA-----GYAGCRVAVTFVLYFLA 292

QY 249 TNYVILVEGLYHLNLIIFVAPFSDTKYLGWFTLIGWGPAAFAVAWAVARATLADARCEW 308
Db 293 TNYVILVEGLYHLNLIIFVAPFSDTKYLGWFTLIGWGPAAFAVAWAVARATLADARCEW 352

QY 309 LSAGDIKTIYQAPILAAIGLNFILFLNTVRVLAIGLNFILFLNTVRVLAIGLNFILFLNT 368
Db 353 LSSGNGKWIIOVPILAAIWNFILFINIIRVLAIGLNFILFLNTVRVLAIGLNFILFLNT 412

QY 369 VLVFGVHIVFVCLPHS--FTGLGWEIFRMHCLIFVAPFSDTKYLGWFTLIGWGPAAFAVA 427
Db 413 MFLFVGHVHIVFVCLPHS--FTGLGWEIFRMHCLIFVAPFSDTKYLGWFTLIGWGPAAFAVA 472

QY 428 WSRNLSVDKRTTPCGSRRCGSLVLTITVTHSTSSQSOVAAAHAWCLSLAKLPRSPADSIT 487
Db 473 WSRWTLALDFKKKARSGSSY-SYGPMTVSHTSVTNVGPRAGLGLPLSPRLPAAATTTA 531

QY 488 ATSLYLAWSGVTVQRTASHTL-----STRNKED-----SGRORDIILMEKPSRPMES 535
Db 532 TTNGHPPIPGHT--KPGAPTLFATPPATAAPKDDGFLNGSCGLDEEASAPERPPALLQE 589

QY 536 NPDT 539
Db 590 EWET 593

RESULT 10
US-09-943-446-9
; Sequence 9, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PCI0891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170

;; PRIOR FILING DATE: 2000-08-30
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9
;; LENGTH: 593
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-943-446-9

Query Match 46.0%; Score 1336.5; DB 10; Length 593;
Best Local Similarity 47.4%; Pred. No. 3.9e-123;
Matches 276; Conservative 81; Mismatches 134; Indels 91; Gaps 11;
QY 22 ARAQLSDGTTIEEQIVLVKAKVQCELMNITAQQL----- 57
DB 22 AYALVDADDVMTKEEQIFLLHRAQAQCEKELKEVLQRPASIMESDKGWTSASTSGKPRKD 81
QY 58 -----EGEN----- 57
DB 82 KASGLYPESEEDKEAPTGSRYGRPCLPEDWDHILCWPLGAPGEVAVPCPDYIDFNHK 141
QY 97 GVAFRHCNPNGTWDFMHSLNKTNWYSDCLRFQPDISIGKQFCERLYVMYTVGYISIF 156
DB 142 GHAYRCDRNGMELVPCHNRTWYSECYKFLTNETR--EREVDFRLGMIYTVGYISVL 199
QY 157 GSLAVAILIIGYFRRLHCTRNYYHMLFVSPMLRATSI FVKDRVVAHIGVKELESJ---- 213
DB 200 ASLTVAVLILAYFRRLHCTRNYYHMLFSLFMLRAVSI FVKDAVLYSGATLDEAERLTEE 259
QY 214 ----IMODDPONS TEATSVDKSYGICKIAVMVFYFLATNYWILVEGLYHLNLI FVAF 269
DB 260 ELRAIAQAPPPATAAG-----YAGCRVATFPLFLATNYWILVEGLYHLNLI FMAF 314
QY 270 FSDTKYLWGFTLIGWGFPAFAVAWAVARATLADARCWELSGADIKWYQAPILAAIGLN 329
DB 315 FSEKKYLWGFTVFGWGLPAVEFAVWVSVRATLANTGCDLSSGNKKWIIQVPIIASIVLN 374
QY 330 FILFNTVRVLATKIWETNAVGHDTROYRKLAKSTLVLVPGVHVIVFVCLPHS-FTG 388
DB 375 FILFINVRVLATKRLNAGRCRTROYRKLKSTLVLMLPLFGVHVIVFMATPYTEVSG 434
QY 389 LGWEIRMHCELFNFSFQGFVSIICYCNGEVOAEVKMMSRWNLSDVKRTPPCGSRRC 448
DB 435 TLWQVQMYHEMLNFSFQGFVAILIYCFCNGEVOAEIKKMSRWTLALDPKPKARSGSSSY 494
QY 449 G-SVLTTVTHSTSSQSOVAHAHAWCLSLAKLPRSPADSLTATSL-YLAMSGVTSQRT-AS 505
DB 495 SYGPMVSHTSVTNVPVGLG-----LPLSPRLPTATTNGHPQLPGHAKPGT PAL 545
QY 506 HTLSTRS-----NKEDSGRORDDILMEK 528
DB 546 ETLTTPPAMAPKDDGFLNGSCSGLDEEASGPERPPALQOE 587

RESULT 11

US-10-225-567A-229
;; Sequence 229, Application US/10225567A
;; Publication No. US20030113798A1
;; GENERAL INFORMATION:
;; APPLICANT: LifeSpan Biosciences
;; APPLICANT: Brown, Joseph P.
;; APPLICANT: Burner, Glenn C.
;; APPLICANT: Roush, Christine L.
;; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
;; FILE REFERENCE: 1920-4-4
;; CURRENT APPLICATION NUMBER: US/10/225,567A
;; CURRENT FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 60/257,144
;; PRIOR FILING DATE: 2000-12-19
;; NUMBER OF SEQ ID NOS: 2292
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 229
;; LENGTH: 593

;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-225-567A-229

Query Match 45.0%; Score 1336.5; DB 15; Length 593;
Best Local Similarity 47.4%; Pred. No. 3.9e-123;
Matches 276; Conservative 81; Mismatches 134; Indels 91; Gaps 11;
QY 22 ARAQLSDGTTIEEQIVLVKAKVQCELMNITAQQL----- 57
DB 22 AYALVDADDVMTKEEQIFLLHRAQAQCEKELKEVLQRPASIMESDKGWTSASTSGKPRKD 81
QY 58 -----EGEN----- 57
DB 82 KASGLYPESEEDKEAPTGSRYGRPCLPEDWDHILCWPLGAPGEVAVPCPDYIDFNHK 141
QY 97 GVAFRHCNPNGTWDFMHSLNKTNWYSDCLRFQPDISIGKQFCERLYVMYTVGYISIF 156
DB 142 GHAYRCDRNGMELVPCHNRTWYSECYKFLTNETR--EREVDFRLGMIYTVGYISVL 199
QY 157 GSLAVAILIIGYFRRLHCTRNYYHMLFVSPMLRATSI FVKDRVVAHIGVKELESJ---- 213
DB 200 ASLTVAVLILAYFRRLHCTRNYYHMLFSLFMLRAVSI FVKDAVLYSGATLDEAERLTEE 259
QY 214 ----IMODDPONS TEATSVDKSYGICKIAVMVFYFLATNYWILVEGLYHLNLI FVAF 269
DB 260 ELRAIAQAPPPATAAG-----YAGCRVATFPLFLATNYWILVEGLYHLNLI FMAF 314
QY 270 FSDTKYLWGFTLIGWGFPAFAVAWAVARATLADARCWELSGADIKWYQAPILAAIGLN 329
DB 315 FSEKKYLWGFTVFGWGLPAVEFAVWVSVRATLANTGCDLSSGNKKWIIQVPIIASIVLN 374
QY 330 FILFNTVRVLATKIWETNAVGHDTROYRKLAKSTLVLVPGVHVIVFVCLPHS-FTG 388
DB 375 FILFINVRVLATKRLNAGRCRTROYRKLKSTLVLMLPLFGVHVIVFMATPYTEVSG 434
QY 389 LGWEIRMHCELFNFSFQGFVSIICYCNGEVOAEVKMMSRWNLSDVKRTPPCGSRRC 448
DB 435 TLWQVQMYHEMLNFSFQGFVAILIYCFCNGEVOAEIKKMSRWTLALDPKPKARSGSSSY 494
QY 449 G-SVLTTVTHSTSSQSOVAHAHAWCLSLAKLPRSPADSLTATSL-YLAMSGVTSQRT-AS 505
DB 495 SYGPMVSHTSVTNVPVGLG-----LPLSPRLPTATTNGHPQLPGHAKPGT PAL 545
QY 506 HTLSTRS-----NKEDSGRORDDILMEK 528
DB 546 ETLTTPPAMAPKDDGFLNGSCSGLDEEASGPERPPALQOE 587

RESULT 12

US-09-943-446-7
;; Sequence 7, Application US/09943446
;; Patent No. US20020146777A1
;; GENERAL INFORMATION:
;; APPLICANT: Pfizer Inc.
;; APPLICANT: Castleberry, Tessa A.
;; APPLICANT: Lu, Bihong
;; APPLICANT: Owen, Thomas A.
;; APPLICANT: Smock, Steven L.
;; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
;; FILE REFERENCE: PCI0891AGER
;; CURRENT APPLICATION NUMBER: US/09/943,446
;; CURRENT FILING DATE: 2001-08-30
;; PRIOR APPLICATION NUMBER: US 60/229,170
;; PRIOR FILING DATE: 2000-08-30
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 7
;; LENGTH: 591
;; TYPE: PRT
;; ORGANISM: Rattus No. US20020146777A1vegicus
US-09-943-446-7

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22 22 ARAGLSDSGHITIBEQIVLVLKAKYQCE-----LNTAQLOQEGN----- 62
22 22 AYALVDADDVFTKEBQIFLHRAQAQCCKLLKEVLHHTAANIMESDKGWTASTSGKPRKE 81
63 63 -----CFPEWDGLICWPRGTGVGKISAVPCPPYITDFNHHK 96
82 82 KASGKFYPESKENKDVPCTGSRRRGRFCLPEWDNICWPLGAPGVAWVPCPDYIDFNHK 141
97 97 GVAFRHCNPNGTDFWHSJLNKTWANSOCLRPLQPDISIGKQECERLYVMYTVGYISIF 156
142 142 GHATRCORNGSEVVPGRHNRWANSYSECLKFWMTETR--BREVDFRLGMIYTVGYISWML 199
157 157 GSLAVAILIIGYFRRRLHCTRNYIHMHLFVSFMLRATSIFVRDQVYVHAHIGYKELES!-- 213
200 200 ASLTVAVLILAYFRRRLHCTRNYIHMHFLSFMRLAASIFVMDVLYSGFTLDEARLTEE 259
214 214 ----IMODDPQNSIEATSDKSOYIGCKTAVVMFIVFLATNYMLVEGLYHLNLIEMAF 269
260 260 ELHIIAQVPPPPAAAANG-----YAGCRVAVTFFIYFLATNYMLVEGLYHLNLIEMAF 314
270 270 PSDTKYUWGFIITGWGPPAFVAANAVARATLADARCWELSGADIKMIIQAPILAAJGLN 329
315 315 FSEKXYLWGFTIFGWGLPAFVAVVGVVRATLANTGCWDLSSGHKKMIIQVPIILASVULN 374
330 330 FILFINTVRVLAKIWMETNAVGHDTKQYRKAKSLTLVLVLVFGVHYIVFVCLPHS--FTG 388
375 375 FILFINIIRVLATKLRETNAGRCDTRQYRKLLRSTLVLVLVPLFGVHYIVFVMAFPYEVSG 434
389 389 LGWIRMHCELFPNSFGQFPVSTIICYCNGEVQOAEVKQWSEWLSVDWKEPTPGSGRRCC 448
435 435 TLMQIOHMYELMNSFGQFVAILIYCFNCEVQOABIRKWSRWTLALDFKKRKARSGSSY 494
449 449 GSVLTITVTHSTSSQOAAAHAWCLSLAKLRPSADSLTATSLYLAMSG-----VTQS 501
495 495 -SYGPMVSHSTVTVNGVRAG-----LSLPLSERLPP--ATTNGHSQLPGHAKPGAPATET 546
502 502 RTASHTLSTRS-----NKEDSGRQRDDIIMEX 528
547 547 ETLPVMTAVPKDGFINGSCGLDEERASGARPPPLLOE 565

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; Sequence ZI, Application US710286730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-267-730-21

Query Match          45.8%; Score 1331.5; DB 12; Length 593;
Best Local Similarity 47.4%; Pred. No. 1.2e-122;
Matches 276; Conservative 80; Mismatches 135; Indels 91; Gaps 11;

QY      22 ARAQLDSGGTTTIEEQIVLVLKAKVOCENLTATQIQ----- 57

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Db 22 AYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRPASIMESDKGWTSASTSGKPRKD 81
QY 58 -----EGGN-----CFPEWDGLICWPRGTGVIKISAVPCPPYIYDNH 96
Db 82 KASGKLYPESEDEKAPTSGRYRGPCLPEWDHILCWPLGAPGEVAVPCPDYIYDNH 141
QY 97 GVAFPHCNPTGTDWFMHSLNKTWANYSDCLFLOPD1SIGQEFCEFLYVMTVGYISIF 156
Db 142 GHAYRRCDRNGSWELVPGHNRWTWANYSECVKFLNETR--EREVDFRLGMIYTVGYSVSL 199
QY 157 GSLAVAILIIGYFRRLHCTRNVIHMLFVSPMLRATSI FVKDRVVHAHIGVKELES--- 213
Db 200 ASLTAVAILIAYFRRLHCTRNVIHMLFVSPMLRAVSI FVKDAVLYSGATLDEAERLTEE 259
QY 214 ----IMODDPONSIEATSVDSKSYIGCKIAVVMFIYFLATNYWILVEGLYHNLIFVAF 269
Db 260 ELRALAQAPPPATAAG-----YAGCRVATFFLYFLATNYWILVEGLYHNLIFMAF 314
QY 270 FSDTKYLWGFILIGWGFPAAFVAWAVARATLADARCWELSGADIKWIYQAPILAAIGLN 329
Db 315 FSEKKYLWGFVFGWGLPAFVAVVWVSVRATLANTGCWDLSSGNKKWIIQVPIIASIVLN 374
QY 330 FILFLNTVRVLATKIWETNAVGHDTKQYRKLAKSTLVLVVFGVHYIVFVCLPHS-FTG 388
Db 375 FILFINIVRVLATKURETNAGRCDFRQYRKLKSLPLVLMPLFGVHYIVFVWATPYTEVSG 434
QY 389 LGWEIRMHCELPFNSFOGFFVSIICYCNGEVOAEVKWMSRNLSVDWKRTPPCGSRRC 448
Db 435 TLWQVQMHYEMLFNSFOGFFVSIICYCNGEVOAEIKKSWRWTALDFFKARSGSSSY 494
QY 449 G-SVLTVTHTSTSSOSQVAAAHAWCLSLAKLPRSPADSLTATSL-YLAMSGVTSQRT-AS 505
Db 495 SYGPMVSHTSVTNUGPRVGLG-----LPLSPRLPTATTNGHPQLPGHAKPGTAL 545
QY 506 HTLSTRS-----NKEDSGRQDDILMEK 528
Db 546 ETLETPPAMAAPKDDGFLNGSCGLDEEASGPERPPALLOE 587

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Search completed: November 21, 2003, 22:33:01
Job time : 37 secs

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RESULT 15
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; Sequence 563, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

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Query Match 45.8%; Score 1330.5; DB 12; Length 593;
Best Local Similarity 47.3%; Pred. No. 1.5e-122;
Matches 275; Conservative 81; Mismatches 135; Indels 91; Gaps 11;

QY 22 ARAQLDSGDTTIEBQIVLVILKAKVQCELNITAQLQ----- 57
Db 22 AYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRPASIMESDKGWTSASTSGKPRKD 81
QY 58 -----EGGN-----CFPEWDGLICWPRGTGVIKISAVPCPPYIYDNH 96

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:26:05 ; Search time 176 Seconds
(without alignments)

2796.966 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 2907

Sequence: 1 MAWLGAHLVWGLMGSL.....DDILMKPSRPWESNPDTEG 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA Main:*

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32: /cgn2_6/prodata1/paa/US60 COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2907	100.0	541	8	US-08-468-011-2

Sequence 2, Appli

2	2907	100.0	541	25	US-09-996-569-2	Sequence 2, Appli
3	2635	90.6	550	1	PCT-US00-21278-20	Sequence 20, Appl
4	2635	90.6	550	20	US-09-631-603-20	Sequence 20, Appl
5	2635	90.6	550	24	US-09-949-004-286	Sequence 286, App
6	2635	90.6	550	27	US-10-126-052A-663	Sequence 663, App
7	2635	90.6	550	28	US-10-225-567A-227	Sequence 227, App
8	2635	90.6	550	28	US-10-295-027-526	Sequence 526, App
9	2635	90.6	550	28	US-10-295-027-851	Sequence 851, App
10	2635	90.6	550	30	US-10-404-618-86	Sequence 86, Appl
11	2629	90.4	550	33	US-09-826-509-565	Sequence 565, App
12	2600	89.4	550	26	US-10-014-162-110	Sequence 110, App
13	2586	89.0	593	32	US-60-245-228-218	Sequence 218, App
14	2586	89.0	593	32	US-60-258-272-90	Sequence 90, Appl
15	2513	86.4	561	27	US-10-126-052A-661	Sequence 661, App
16	2513	86.4	561	28	US-10-295-027-524	Sequence 524, App
17	2213.5	76.1	546	26	US-10-014-162-109	Sequence 109, App
18	2166.5	74.5	546	27	US-10-144-779-319	Sequence 319, App
19	1822	62.7	421	21	US-09-724-676A-82566	Sequence 82566, A
20	1822	62.7	421	21	US-09-724-676A-82566	Sequence 82566, A
21	1672.5	57.5	575	29	US-10-372-095-5	Sequence 5, Appli
22	1493.5	51.4	536	24	US-09-949-004-360	Sequence 360, App
23	1418.5	48.8	536	29	US-10-372-095-2	Sequence 2, Appli
24	1397	48.1	585	13	US-08-935-317-6	Sequence 6, Appli
25	1392	47.9	585	1	PCT-US94-12205-136	Sequence 136, App
26	1392	47.9	585	5	US-08-171-331-14	Sequence 14, Appl
27	1392	47.9	585	8	US-08-455-919-125	Sequence 125, App
28	1392	47.9	585	8	US-08-458-075-125	Sequence 125, App
29	1392	47.9	585	15	US-09-199-874-19	Sequence 19, Appl
30	1392	47.9	585	15	US-09-199-874-19	Sequence 19, Appl
31	1392	47.9	585	15	US-09-199-874-19	Sequence 19, Appl
32	1392	47.9	585	15	US-09-199-874-19	Sequence 19, Appl
33	1392	47.9	585	15	US-09-199-874-19	Sequence 19, Appl
34	1388	47.7	515	15	US-09-199-874-18	Sequence 18, Appl
35	1388	47.7	515	15	US-09-199-874-18	Sequence 18, Appl
36	1388	47.7	515	15	US-09-199-874-18	Sequence 18, Appl
37	1388	47.7	515	15	US-09-199-874-18	Sequence 18, Appl
38	1388	47.7	515	15	US-09-199-874-18	Sequence 18, Appl
39	1370.5	47.1	337	32	US-60-207-317-387	Sequence 387, App
40	1370.5	47.1	337	32	US-60-229-515-1257	Sequence 1257, App
41	1345.5	46.3	595	24	US-09-943-446-6	Sequence 6, Appli
42	1337	46.0	553	21	US-09-724-676A-81959	Sequence 81959, A
43	1337	46.0	553	21	US-09-724-676A-81959	Sequence 81959, A
44	1336.5	46.0	593	1	PCT-US00-21278-21	Sequence 21, Appl
45	1336.5	46.0	593	20	US-09-631-603-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-08-468-011-2

Sequence 2, Application US/08468011

GENERAL INFORMATION:

APPLICANT: Soppet, Daniel R

APPLICANT: Yi, Li

APPLICANT: Rosen, Craig A

APPLICANT: Ruben, Steven

TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor

TITLE OF INVENTION: HLTG74

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,

ADDRESSEE: Stewart & Olstein

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: NJ

COUNTRY: USA

ZIP: 07068-1739

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/468,011
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferraro, Gregory D
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-458
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 541 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-468-011-2

Query Match 100.0%; Score 2907; DB 8; Length 541;
 Best Local Similarity 100.0%; Pred. No. 2.7e-271;
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMLGASLHVGMWMLGSLCLARAQLDSGTITIEEQIVLVKAKVOCELNITIAQLOGE 60
 DB 1 MAMLGASLHVGMWMLGSLCLARAQLDSGTITIEEQIVLVKAKVOCELNITIAQLOGE 60
 QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
 DB 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
 QY 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
 DB 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
 QY 181 MHLFVSPMLRATSI FVKDRVVVHAHIGVKELESIMQDDPONSIEATSVDSKSOYIGCKIAV 240
 DB 181 MHLFVSPMLRATSI FVKDRVVVHAHIGVKELESIMQDDPONSIEATSVDSKSOYIGCKIAV 240
 QY 241 VMIYIFLATNYWILVEGLYLHNLIFVAFPSDTKYLWGFLIIGWGFPAAFVAAMAVARAT 300
 DB 241 VMIYIFLATNYWILVEGLYLHNLIFVAFPSDTKYLWGFLIIGWGFPAAFVAAMAVARAT 300
 QY 301 LADARCWELSGADIKWYQAPILAAIGNLIFLNTVRLATKIWETNAVGHDTKQYRK 360
 DB 301 LADARCWELSGADIKWYQAPILAAIGNLIFLNTVRLATKIWETNAVGHDTKQYRK 360
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 DB 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSGFQGFVFSIIYCYNGEV 420
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 DB 421 QAEVKQWNRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
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 DB 481 SPADSLTATSLYLAMSGVTSRTASHTLSRKNKEDSGRQDDILMEKSPRMESNPDTTE 540
 QY 541 G 541
 DB 541 G 541

RESULT 2
 US-09-996-569-2
 ; Sequence 2, Application US/09996569
 ; GENERAL INFORMATION:
 ; APPLICANT: Soppet et al.
 ; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
 ; FILE REFERENCE: PF201D1
 ; CURRENT APPLICATION NUMBER: US/09/996,569
 ; CURRENT FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 08/468,011
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 541
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-996-569-2

Query Match 100.0%; Score 2907; DB 25; Length 541;
 Best Local Similarity 100.0%; Pred. No. 2.7e-271;
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMLGASLHVGMWMLGSLCLARAQLDSGTITIEEQIVLVKAKVOCELNITIAQLOGE 60
 DB 1 MAMLGASLHVGMWMLGSLCLARAQLDSGTITIEEQIVLVKAKVOCELNITIAQLOGE 60
 QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
 DB 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
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 DB 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
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 DB 181 MHLFVSPMLRATSI FVKDRVVVHAHIGVKELESIMQDDPONSIEATSVDSKSOYIGCKIAV 240
 QY 241 VMIYIFLATNYWILVEGLYLHNLIFVAFPSDTKYLWGFLIIGWGFPAAFVAAMAVARAT 300
 DB 241 VMIYIFLATNYWILVEGLYLHNLIFVAFPSDTKYLWGFLIIGWGFPAAFVAAMAVARAT 300
 QY 301 LADARCWELSGADIKWYQAPILAAIGNLIFLNTVRLATKIWETNAVGHDTKQYRK 360
 DB 301 LADARCWELSGADIKWYQAPILAAIGNLIFLNTVRLATKIWETNAVGHDTKQYRK 360
 QY 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSGFQGFVFSIIYCYNGEV 420
 DB 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSGFQGFVFSIIYCYNGEV 420
 QY 421 QAEVKQWNRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
 DB 421 QAEVKQWNRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
 QY 481 SPADSLTATSLYLAMSGVTSRTASHTLSRKNKEDSGRQDDILMEKSPRMESNPDTTE 540
 DB 481 SPADSLTATSLYLAMSGVTSRTASHTLSRKNKEDSGRQDDILMEKSPRMESNPDTTE 540
 QY 541 G 541
 DB 541 G 541

RESULT 3
 PCT-US00-21278-20
 ; Sequence 20, Application PC/TUS0021278
 ; GENERAL INFORMATION:
 ; APPLICANT: Hodge, Martin R.
 ; APPLICANT: Lloyd, Clare
 ; APPLICANT: Weich, Nadine
 ; TITLE OF INVENTION: 15571, A Novel GPCR-like Molecule of the
 ; TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
 ; FILE REFERENCE: 5800-48A
 ; CURRENT APPLICATION NUMBER: PCT/US00/21278
 ; CURRENT FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 09/515,781
 ; PRIOR FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: 60/146,916
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 20
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-21278-20

Query Match 90.6%; Score 2635; DB 1; Length 550;
Best Local Similarity 91.4%; Pred. No. 5.7e-245;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

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DB 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGFFVSIYCY 420
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DB 421 QAEVKWMSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL 477
QY 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKSP 534
DB 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKSP 534
QY 535 SNPDTEG 541
DB 535 SNPDTEG 541

RESULT 4

US-09-631-603-20
; Sequence 20, Application US/09631603
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Claire
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: 15571, A Novel GPCR-like Molecule of the
; TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
; FILE REFERENCE: 5800-48A
; CURRENT APPLICATION NUMBER: US/09/631,603
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/515,781
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-631-603-20

Query Match 90.6%; Score 2635; DB 20; Length 550;
Best Local Similarity 91.4%; Pred. No. 5.7e-245;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

QY 1 MAMLGASLHVWGLMGLSCLLARAQLDSGTITIEEQIVLVKAKVQCELNITAOQE 60
DB 1 MAGLGASLHVWGLMGLSCLLARAQLDSGTITIEEQIVLVKAKVQCELNITAOQE 60
QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNK 120
DB 61 GNCPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNK 120
QY 121 NYSCLRFLOPDISIGKQEFCELYVWYTVGYSISFGSLAVAILIIGYFRLLHCTRN 180
DB 121 NYSCLRFLOPDISIGKQEFCELYVWYTVGYSISFGSLAVAILIIGYFRLLHCTRN 180
QY 181 MHLFVSMRLRATSIKQEFCELYVWYTVGYSISFGSLAVAILIIGYFRLLHCTRN 240
DB 181 MHLFVSMRLRATSIKQEFCELYVWYTVGYSISFGSLAVAILIIGYFRLLHCTRN 240
QY 241 VMEIYFLATNYWYLLVEGLYLHNLIFVAFSDTKYLMGFILGWGFPAAFAVA 300
DB 241 VMEIYFLATNYWYLLVEGLYLHNLIFVAFSDTKYLMGFILGWGFPAAFAVA 300
QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILNTVRLATKIWETNAVGHDTKQYRK 360
DB 301 LADARCWELSGADIKWYQAPILAAIGLNFILNTVRLATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGFFVSIYCY 420
DB 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGFFVSIYCY 420
QY 421 QAEVKWMSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL 477
DB 421 QAEVKWMSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL 477
QY 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKSP 534
DB 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKSP 534
QY 535 SNPDTEG 541
DB 535 SNPDTEG 541

RESULT 5

US-09-949-004-286
; Sequence 286, Application US/09949004
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000848
; CURRENT APPLICATION NUMBER: US/09/949,004
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/232,045
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 6961
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Human
US-09-949-004-286

Query Match 90.6%; Score 2635; DB 24; Length 550;
Best Local Similarity 91.4%; Pred. No. 5.7e-245;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

QY 1 MAMLGASLHVWGLMGLSCLLARAQLDSGTITIEEQIVLVKAKVQCELNITAOQE 60

Db 1 MAGLGASLHVWMLGSLCLARALQSDGTTIEEQIVLVKAKVQCELNITAQLOE 60
QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHNCNPNGTWDFMHSNKTWA 120
Db 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHNCNPNGTWDFMHSNKTWA 120
QY 121 NYSCLRFLOPDISIGKQFCERLYYMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
Db 121 NYSCLRFLOPDISIGKQFCERLYYMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
QY 181 MHLFVSFMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKQYIGCKIAV 240
Db 181 MHLFVSFMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKQYIGCKIAV 240
QY 241 VMFIYFLATNYWILVEGLYLNLI FVAFSDTKYLMGFLILGWGPPAAFAVAWAVARAT 300
Db 241 VMFIYFLATNYWILVEGLYLNLI FVAFSDTKYLMGFLILGWGPPAAFAVAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDRKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDRKQYRK 360
QY 361 LAKSTLVLVFGVHYIYFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVFGVHYIYFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKQWNRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
Db 421 QAEVKQWNRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
QY 478 LPRSPADSLTATSLYLAAMSGVTQSRASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
Db 478 LPRSPADSLTATSLYLAAMSGVTQSRASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
QY 535 SNPDTGEG 541
Db 535 SNPDTGEG 541

RESULT 6
US-10-126-052A-663
; Sequence 663, Application US/10126052A
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Murray, Richard
; TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Lung Cancer
; FILE REFERENCE: 018501-001530US
; CURRENT APPLICATION NUMBER: US/10/126,052A
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/284,770
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/290,492
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 60/339,245
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/334,370
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 691
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 663
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-126-052A-663

Query Match 90.6%; Score 2635; DB 27; Length 550;

Best Local Similarity 91.4%; Pred. No. 5.7e-245;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;
QY 1 MAGLGASLHVWMLGSLCLARALQSDGTTIEEQIVLVKAKVQCELNITAQLOE 60
Db 1 MAGLGASLHVWMLGSLCLARALQSDGTTIEEQIVLVKAKVQCELNITAQLOE 60
QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHNCNPNGTWDFMHSNKTWA 120
Db 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHNCNPNGTWDFMHSNKTWA 120
QY 121 NYSCLRFLOPDISIGKQFCERLYYMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
Db 121 NYSCLRFLOPDISIGKQFCERLYYMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
QY 181 MHLFVSFMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKQYIGCKIAV 240
Db 181 MHLFVSFMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKQYIGCKIAV 240
QY 241 VMFIYFLATNYWILVEGLYLNLI FVAFSDTKYLMGFLILGWGPPAAFAVAWAVARAT 300
Db 241 VMFIYFLATNYWILVEGLYLNLI FVAFSDTKYLMGFLILGWGPPAAFAVAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDRKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDRKQYRK 360
QY 361 LAKSTLVLVFGVHYIYFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVFGVHYIYFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKQWNRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
Db 421 QAEVKQWNRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
QY 478 LPRSPADSLTATSLYLAAMSGVTQSRASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
Db 478 LPRSPADSLTATSLYLAAMSGVTQSRASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
QY 535 SNPDTGEG 541
Db 535 SNPDTGEG 541

RESULT 7
US-10-225-567A-227
; Sequence 227, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-227

Query Match 90.6%; Score 2635; DB 28; Length 550;
Best Local Similarity 91.4%; Pred. No. 5.7e-245;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;
QY 1 MAGLGASLHVWMLGSLCLARALQSDGTTIEEQIVLVKAKVQCELNITAQLOE 60
Db 1 MAGLGASLHVWMLGSLCLARALQSDGTTIEEQIVLVKAKVQCELNITAQLOE 60

QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDHNHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
 Db 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDHNHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
 QY 121 NYSDCLRFLOPDISIGKQFCEERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYYIH 180
 Db 121 NYSDCLRFLOPDISIGKQFCEERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYYIH 180
 QY 181 MHLFVFSFMLRATSIYFKDRVVAHIGVKELESIMODDPQNSIEATSDVKSOYICNGEV 240
 Db 181 MHLFVFSFMLRATSIYFKDRVVAHIGVKELESIMODDPQNSIEATSDVKSOYICNGEV 240
 QY 241 VMEFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFEIRHCELFNSFGQFVSIICYCNGEV 300
 Db 241 VMEFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFEIRHCELFNSFGQFVSIICYCNGEV 300
 QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILNTVRVLATKIWETNAVGHDTKQYRK 360
 Db 301 LADARCWELSGADIKWYQAPILAAIGLNFILNTVRVLATKIWETNAVGHDTKQYRK 360
 QY 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHCELFNSFGQFVSIICYCNGEV 420
 Db 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHCELFNSFGQFVSIICYCNGEV 420
 QY 421 QAEVKQWWSRWNLSDVKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL---SLAK 477
 Db 421 QAEVKQWWSRWNLSDVKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL---SLAK 477
 QY 478 LPRSPADSLTATSLYLAMSGVTSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
 Db 478 LPRSPADSLTATSLYLAMSGVTSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
 QY 535 SNPDTEG 541
 Db 535 SNPDTEG 541

RESULT 8

US-10-295-027-526
 ; Sequence 526, Application US/10295027
 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsberg, Wendy M.
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Hevez, Peter A.
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 ; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
 ; FILE REFERENCE: 018501-012500US
 ; CURRENT APPLICATION NUMBER: US/10/295,027
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: US 09/663,733
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: US 60/350,666
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/335,394
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: US 60/332,464
 ; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: US 60/334,393
 ; PRIOR FILING DATE: 2001-11-29
 ; PRIOR APPLICATION NUMBER: US 60/340,376
 ; PRIOR FILING DATE: 2001-12-14
 ; PRIOR APPLICATION NUMBER: US 60/347,211
 ; PRIOR FILING DATE: 2002-01-08
 ; PRIOR APPLICATION NUMBER: US 60/347,349
 ; PRIOR FILING DATE: 2002-01-10

; PRIOR APPLICATION NUMBER: US 60/355,250
 ; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: US 60/356,714
 ; PRIOR FILING DATE: 2002-02-13
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1386
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 526
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-295-027-526

Query Match 90.6%; Score 2635; DB 28; Length 550;
 Best Local Similarity 91.4%; Pred. No. 5.7e-245;
 Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;
 QY 1 MAMGASLHVWGMILGSCILLARAQLDSGTITIEBQIVLVLKAKVQCELNITAIQLQEGE 60
 Db 1 MAMGASLHVWGMILGSCILLARAQLDSGTITIEBQIVLVLKAKVQCELNITAIQLQEGE 60
 QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDHNHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
 Db 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDHNHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
 QY 121 NYSDCLRFLOPDISIGKQFCEERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYYIH 180
 Db 121 NYSDCLRFLOPDISIGKQFCEERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYYIH 180
 QY 181 MHLFVFSFMLRATSIYFKDRVVAHIGVKELESIMODDPQNSIEATSDVKSOYICNGEV 240
 Db 181 MHLFVFSFMLRATSIYFKDRVVAHIGVKELESIMODDPQNSIEATSDVKSOYICNGEV 240
 QY 241 VMEFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFEIRHCELFNSFGQFVSIICYCNGEV 300
 Db 241 VMEFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFEIRHCELFNSFGQFVSIICYCNGEV 300
 QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILNTVRVLATKIWETNAVGHDTKQYRK 360
 Db 301 LADARCWELSGADIKWYQAPILAAIGLNFILNTVRVLATKIWETNAVGHDTKQYRK 360
 QY 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHCELFNSFGQFVSIICYCNGEV 420
 Db 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHCELFNSFGQFVSIICYCNGEV 420
 QY 421 QAEVKQWWSRWNLSDVKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL---SLAK 477
 Db 421 QAEVKQWWSRWNLSDVKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL---SLAK 477
 QY 478 LPRSPADSLTATSLYLAMSGVTSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
 Db 478 LPRSPADSLTATSLYLAMSGVTSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
 QY 535 SNPDTEG 541
 Db 535 SNPDTEG 541

RESULT 9

US-10-295-027-851
 ; Sequence 851, Application US/10295027
 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsberg, Wendy M.
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Hevez, Peter A.
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

;; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
;; FILE REFERENCE: 018501-012500US
;; CURRENT APPLICATION NUMBER: US/10/295,027
;; CURRENT FILING DATE: 2002-11-13
;; PRIOR APPLICATION NUMBER: US 09/663,733
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: US 60/350,666
;; PRIOR FILING DATE: 2001-11-13
;; PRIOR APPLICATION NUMBER: US 60/335,394
;; PRIOR FILING DATE: 2001-11-15
;; PRIOR APPLICATION NUMBER: US 60/332,464
;; PRIOR FILING DATE: 2001-11-21
;; PRIOR APPLICATION NUMBER: US 60/334,393
;; PRIOR FILING DATE: 2001-11-29
;; PRIOR APPLICATION NUMBER: US 60/340,376
;; PRIOR FILING DATE: 2001-12-14
;; PRIOR APPLICATION NUMBER: US 60/347,211
;; PRIOR FILING DATE: 2002-01-08
;; PRIOR APPLICATION NUMBER: US 60/347,349
;; PRIOR FILING DATE: 2002-01-10
;; PRIOR APPLICATION NUMBER: US 60/355,250
;; PRIOR FILING DATE: 2002-02-08
;; PRIOR APPLICATION NUMBER: US 60/356,714
;; PRIOR FILING DATE: 2002-02-13
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1386
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 851
;; LENGTH: 550
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-295-027-851

Query Match 90.6%; Score 2635; DB 28; Length 550;
Best Local Similarity 91.4%; Pred. No. 5.7e-245;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

Qy 1 MAMLGASLHVWGLMGLSCLLARAQLDSGTITIEQIVLVKAKVOCELNITAOQE 60
Db 1 MAGLGASLHVWGLMGLSCLLARAQLDSGTITIEQIVLVKAKVOCELNITAOQE 60

Qy 61 GNCPEWDGLICWPRTGVKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNK 120
Db 61 GNCPEWDGLICWPRTGVKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNK 120

Qy 121 NYSDCURFLQPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCT 180
Db 121 NYSDCURFLQPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCT 180

Qy 181 MHLFVSPMLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVKSYIGCKIAV 240
Db 181 MHLFVSPMLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVKSYIGCKIAV 240

Qy 241 VMFIYFLATNYMILVEGLYHLNLI FVAFFSDTKYLMGFLICWGFPAFAVAWAVARAT 300
Db 241 VMFIYFLATNYMILVEGLYHLNLI FVAFFSDTKYLMGFLICWGFPAFAVAWAVARAT 300

Qy 301 LADARCWELSGADIKWYQAPILAAIGLNFILNTVRVLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWYQAPILAAIGLNFILNTVRVLATKIWETNAVGHDTKQYRK 360

Qy 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSGFQGFVSIICYNGEV 420
Db 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSGFQGFVSIICYNGEV 420

Qy 421 QAEVKQWRSWNLVSDWKRTPPCGSRRCGSLVLTTHSTSSQOVAHAWCL---SLAK 477
Db 421 QAEVKQWRSWNLVSDWKRTPPCGSRRCGSLVLTTHSTSSQOVAHAWCL---SLAK 477

Qy 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKSPRME 534
Db 481 IASRQPDSD-----HITLPGYVWSNSEQDCLPHSFHEETKEDSGRQDDILMEKSPRME 534

Qy 535 SNPDTEG 541
Db 535 SNPDTEG 541

RESULT 10
US-10-404-618-86
;; Sequence 86, Application US/10404618
;; GENERAL INFORMATION:
;; APPLICANT: Hodge, Martin R.
;; APPLICANT: Lloyd, Clare M.
;; APPLICANT: Weich, Nadine S.
;; APPLICANT: Lora, Jose M.
;; APPLICANT: White, David
;; APPLICANT: Glucksmann, Maria A.
;; APPLICANT: Robison, Keith E.
;; APPLICANT: Silos-Santiago, Inmaculada
;; APPLICANT: Goodearl, Andrew D.J.
;; APPLICANT: Curtis, Rory A.J.
;; TITLE OF INVENTION: NOVEL 15571, 2465, 14266, 2882, 52871,
;; TITLE OF INVENTION: 8203 AND 16852 MOLECULES AND USES THEREFOR
;; FILE REFERENCE: MPI03-0530MINIM
;; CURRENT APPLICATION NUMBER: US/10/404,618
;; CURRENT FILING DATE: 2003-04-01
;; PRIOR APPLICATION NUMBER: 09/631,603
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: 09/515,781
;; PRIOR FILING DATE: 2000-02-29
;; PRIOR APPLICATION NUMBER: 60/146,916
;; PRIOR FILING DATE: 1999-08-03
;; PRIOR APPLICATION NUMBER: 09/794,763
;; PRIOR FILING DATE: 2001-02-26
;; PRIOR APPLICATION NUMBER: 60/185,942
;; PRIOR FILING DATE: 2000-02-29
;; PRIOR APPLICATION NUMBER: 09/634,392
;; PRIOR FILING DATE: 2000-08-09
;; PRIOR APPLICATION NUMBER: 09/176,075
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 09/013,634
;; PRIOR FILING DATE: 1998-01-26
;; PRIOR APPLICATION NUMBER: 09/884,430
;; PRIOR FILING DATE: 2001-06-18
;; PRIOR APPLICATION NUMBER: 60/269,758
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 96
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 86
;; LENGTH: 550
;; TYPE: PRT
;; ORGANISM: Homo Sapiens
US-10-404-618-86

Query Match 90.6%; Score 2635; DB 30; Length 550;
Best Local Similarity 91.4%; Pred. No. 5.7e-245;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

Qy 1 MAMLGASLHVWGLMGLSCLLARAQLDSGTITIEQIVLVKAKVOCELNITAOQE 60
Db 1 MAGLGASLHVWGLMGLSCLLARAQLDSGTITIEQIVLVKAKVOCELNITAOQE 60

Qy 61 GNCPEWDGLICWPRTGVKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNK 120
Db 61 GNCPEWDGLICWPRTGVKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNK 120

Qy 121 NYSDCURFLQPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCT 180
Db 121 NYSDCURFLQPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCT 180

Qy 181 MHLFVSPMLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVKSYIGCKIAV 240
Db 181 MHLFVSPMLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVKSYIGCKIAV 240

QY 241 VMFIYFLATNYWILVEGLYHLNLIIFVAFPSDTKYLWGLFILLIGWGPFAAFVAWAVARAT 300
DB 241 VMFIYFLATNYWILVEGLYHLNLIIFVAFPSDTKYLWGLFILLIGWGPFAAFVAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYRK 360
DB 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYRK 360
QY 361 LAKSTLVLVFVGVHYIVFVCLPHSFTGLGWEIRMECELFNFSFGQFFVSIYCYCNGEV 420
DB 361 LAKSTLVLVFVGVHYIVFVCLPHSFTGLGWEIRMECELFNFSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
DB 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
QY 478 LPRSPADSLTATSLYLAWSGVTSRTASHTLS---TRSNKEDSGRORDILMEKPSRPM 534
DB 478 LPRSPADSLTATSLYLAWSGVTSRTASHTLS---TRSNKEDSGRORDILMEKPSRPM 534
QY 535 SNPDTEG 541
DB 535 SNPDTEG 541

RESULT 11

US-09-826-509-565
; Sequence 565, Application US/09826509
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 565
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-565

Query Match 90.4%; Score 2629; DB 23; Length 550;
Best Local Similarity 91.2%; Pred. No. 2.2e-244;
Matches 499; Conservative 6; Mismatches 30; Indels 12; Gaps 3;
QY 1 MAMLGASLHVWGLMGLSCLLARALDSDGTITIEQIVLVKAKVQCELNITAQLQEGE 60
DB 1 MAMLGASLHVWGLMGLSCLLARALDSDGTITIEQIVLVKAKVQCELNITAQLQEGE 60
QY 61 GNCPPWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPGTWDPMHSLNKTWA 120
DB 61 GNCPPWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPGTWDPMHSLNKTWA 120
QY 121 NYSCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
DB 121 NYSCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
QY 181 MHLFVSMRLATSIFVKDRVVAHIGVKELESIMODDPONSTEATSVKSOYIGCKIAV 240
DB 181 MHLFVSMRLATSIFVKDRVVAHIGVKELESIMODDPONSTEATSVKSOYIGCKIAV 240
QY 241 VMFIYFLATNYWILVEGLYHLNLIIFVAFPSDTKYLWGLFILLIGWGPFAAFVAWAVARAT 300
DB 241 VMFIYFLATNYWILVEGLYHLNLIIFVAFPSDTKYLWGLFILLIGWGPFAAFVAWAVARAT 300

QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYRK 360
DB 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYRK 360
QY 361 LAKSTLVLVFVGVHYIVFVCLPHSFTGLGWEIRMECELFNFSFGQFFVSIYCYCNGEV 420
DB 361 LAKSTLVLVFVGVHYIVFVCLPHSFTGLGWEIRMECELFNFSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
DB 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
QY 478 LPRSPADSLTATSLYLAWSGVTSRTASHTLS---TRSNKEDSGRORDILMEKPSRPM 534
DB 478 LPRSPADSLTATSLYLAWSGVTSRTASHTLS---TRSNKEDSGRORDILMEKPSRPM 534
QY 535 SNPDTEG 541
DB 535 SNPDTEG 541

RESULT 12

US-10-014-162-110
; Sequence 110, Application US/10014162
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-162-110

Query Match 89.4%; Score 2600; DB 26; Length 550;
Best Local Similarity 90.9%; Pred. No. 1.4e-241;
Matches 498; Conservative 6; Mismatches 30; Indels 14; Gaps 5;
QY 1 MAMLGASLHVWGLMGLSCLLARALDSDGTITIEQIVLVKAKVQCELNITAQLQEGE 60
DB 1 MAMLGASLHVWGLMGLSCLLARALDSDGTITIEQIVLVKAKVQCELNITAQLQEGE 60
QY 61 GNCPPWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPGTWDPMHSLNKTWA 120
DB 61 GNCPPWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPGTWDPMHSLNKTWA 120
QY 121 NYSCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
DB 121 NYSCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
QY 181 MHLFVSMRLATSIFVKDRVVAHIGVKELESIMODDPONSTEATSVKSOYIGCKIA 239
DB 181 MHLFVSMRLATSIFVKDRVVAHIGVKELESIMODDPONSTEATSVKSOYIGCKIA 240
QY 240 VMFIYFLATNYWILVEGLYHLNLIIFVAFPSDTKYLWGLFILLIGWGPFAAFVAWAVARAT 299
DB 240 VMFIYFLATNYWILVEGLYHLNLIIFVAFPSDTKYLWGLFILLIGWGPFAAFVAWAVARAT 299
QY 300 TLADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYR 359
DB 300 TLADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYR 359
QY 360 KLAESTLVLVFVGVHYIVFVCLPHSFTGLGWEIRMECELFNFSFGQFFVSIYCYCNGE 419
DB 360 KLAESTLVLVFVGVHYIVFVCLPHSFTGLGWEIRMECELFNFSFGQFFVSIYCYCNGE 419

Db 360 KLAKSTLVLVVFGVHYVFCVCLPHSFTGLGWEIRHMCLEFPNSFQGFVSVIICYCNGE 419
 Qy 420 VQAEVKKWSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLA 476
 Db 420 VQAEVKKWSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLA 479
 Qy 477 LPRSPADSLTATSLYVGLVMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 533
 Db 480 KIASRQPDSD-----HITLPGVWNSQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 533
 Qy 534 ESNPDTEG 541
 Db 534 ESNPDTEG 541

RESULT 13

US-60-245-228-218
 ; Sequence 218, Application US/60245228
 ; GENERAL INFORMATION:
 ; APPLICANT: Beasley, Ellen
 ; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL000878
 ; CURRENT APPLICATION NUMBER: US/60/245,228
 ; CURRENT FILING DATE: 2000-11-03
 ; NUMBER OF SEQ ID NOS: 630
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 218
 ; LENGTH: 593
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 US-60-245-228-218

Query Match 89.0%; Score 2586; DB 32; Length 593;
 Best Local Similarity 90.5%; Pred. No. 3.5e-240;
 Matches 495; Conservative 6; Mismatches 30; Indels 16; Gaps 5;

Qy 1 MAWLGLSLHYVWGLMGLSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITAIQOGE 60
 Db 48 MAGLGLSLHYVWGLMGLSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITAIQOGE 107
 Qy 61 GNCPEWDGLICWPGRGTGKISAVPCPPYIYDFNHKGVAFRHCPNPGTDFMHSLNKTWA 120
 Db 108 GNCPEWDGLICWPGRGTGKISAVPCPPYIYDFNHKGVAFRHCPNPGTDFMHSLNKTWA 167
 Qy 121 NYSCLRFLOPDISIGKQEFCELYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
 Db 168 NYSCLRFLOPDISIGKQEFCELYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 227
 Qy 181 MHLFVSEMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSOYIGCKIAV 240
 Db 228 MHLFVSEMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSOYIGCKIAV 287
 Qy 241 VMEIYFLATNYVYLVEGLYHNLIFVAFPSDTKYLWGFIILGWGFPAAAFVAAWAVARAT 300
 Db 288 VMEIYFLATNYVYLVEGLYHNLIFVAFPSDTKYLWGFIILGWGFPAAAFVAAWAVARAT 345
 Qy 301 LADARCWELSGADIKWYQAPILAAI--QFILFLNTVTVLTKIETNAVGHDTKQYRK 360
 Db 346 LADARCWELSGADIKWYQAPILAAI--QFILFLNTVTVLTKIETNAVGHDTKQYRK 403
 Qy 361 LAKSTLVLVVFGVHYVFCVCLPHSFTGLGWEIRHMCLEFPNSFQGFVSVIICYCNGEV 420
 Db 404 LAKSTLVLVVFGVHYVFCVCLPHSFTGLGWEIRHMCLEFPNSFQGFVSVIICYCNGEV 463
 Qy 421 QAEVKKWSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLAK 477
 Db 464 QAEVKKWSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLAK 523
 Qy 478 LPRSPADSLTATSLYVGLVMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
 Db 524 IASRQPDSD-----HITLPGVWNSQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 577

Qy 535 SNPDTEG 541
 Db 578 SNPDTEG 584

RESULT 14

US-60-258-272-90
 ; Sequence 90, Application US/60258272
 ; GENERAL INFORMATION:
 ; APPLICANT: Beasley, Ellen
 ; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL0001041
 ; CURRENT APPLICATION NUMBER: US/60/258,272
 ; CURRENT FILING DATE: 2000-12-27
 ; NUMBER OF SEQ ID NOS: 252
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 90
 ; LENGTH: 593
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 US-60-258-272-90

Query Match 89.0%; Score 2586; DB 32; Length 593;
 Best Local Similarity 90.5%; Pred. No. 3.5e-240;
 Matches 495; Conservative 6; Mismatches 30; Indels 16; Gaps 5;

Qy 1 MAWLGLSLHYVWGLMGLSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITAIQOGE 60
 Db 48 MAGLGLSLHYVWGLMGLSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITAIQOGE 107
 Qy 61 GNCPEWDGLICWPGRGTGKISAVPCPPYIYDFNHKGVAFRHCPNPGTDFMHSLNKTWA 120
 Db 108 GNCPEWDGLICWPGRGTGKISAVPCPPYIYDFNHKGVAFRHCPNPGTDFMHSLNKTWA 167
 Qy 121 NYSCLRFLOPDISIGKQEFCELYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
 Db 168 NYSCLRFLOPDISIGKQEFCELYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 227
 Qy 181 MHLFVSEMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSOYIGCKIAV 240
 Db 228 MHLFVSEMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSOYIGCKIAV 287
 Qy 241 VMEIYFLATNYVYLVEGLYHNLIFVAFPSDTKYLWGFIILGWGFPAAAFVAAWAVARAT 300
 Db 288 VMEIYFLATNYVYLVEGLYHNLIFVAFPSDTKYLWGFIILGWGFPAAAFVAAWAVARAT 345
 Qy 301 LADARCWELSGADIKWYQAPILAAI--QFILFLNTVTVLTKIETNAVGHDTKQYRK 360
 Db 346 LADARCWELSGADIKWYQAPILAAI--QFILFLNTVTVLTKIETNAVGHDTKQYRK 403
 Qy 361 LAKSTLVLVVFGVHYVFCVCLPHSFTGLGWEIRHMCLEFPNSFQGFVSVIICYCNGEV 420
 Db 404 LAKSTLVLVVFGVHYVFCVCLPHSFTGLGWEIRHMCLEFPNSFQGFVSVIICYCNGEV 463
 Qy 421 QAEVKKWSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLAK 477
 Db 464 QAEVKKWSRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLAK 523
 Qy 478 LPRSPADSLTATSLYVGLVMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
 Db 524 IASRQPDSD-----HITLPGVWNSQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 577
 Qy 535 SNPDTEG 541
 Db 578 SNPDTEG 584

RESULT 15

US-10-126-052A-661
 ; Sequence 661, Application US/10126052A

Search completed: November 21, 2003, 22:31:40
Job time : 178 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 22:23:14 ; Search time 17 Seconds

(without alignments)
1496.556 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 2907

Sequence: 1 MAWLGAHLVWGMGLGSL.....DDILMEKPSRPMESNPDTEG 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2635	90.6	550	1	PTH2 HUMAN
2	2213.5	76.1	546	1	PTH2 RAT
3	1397	48.1	585	1	PTH2 DIDMA
4	1345	46.3	585	1	PTH2 PIG
5	1336.5	46.0	593	1	PTH2 HUMAN
6	1331.5	45.8	591	1	PTH2 RAT
7	1324	45.5	591	1	PTH2 MOUSE
8	801	27.6	449	1	SCRC RAT
9	794	27.3	445	1	SCRC RABIT
10	793	27.3	457	1	VIPR MELGA
11	791.5	27.2	459	1	VIPR MOUSE
12	785	27.0	458	1	VIPR PIG
13	784	27.0	440	1	SCRC HUMAN
14	782	26.9	447	1	VIPR CARAU
15	772.5	26.6	459	1	VIPR RAT
16	759.5	26.1	457	1	VIPR HUMAN
17	713.5	24.5	437	1	VIPR MOUSE
18	708	24.4	437	1	VIPR RAT
19	702	24.1	438	1	VIPR HUMAN
20	685	23.6	468	1	PACR HUMAN
21	677.5	23.3	496	1	PACR MOUSE
22	673.5	23.2	513	1	PACR BOVIN
23	667.5	23.0	523	1	PACR RAT
24	665	22.9	550	1	GLP2 RAT
25	663	22.8	489	1	GLP1 MOUSE
26	662	22.8	462	1	GIPR MESAU
27	655	22.5	463	1	GLP1 RAT
28	641.5	22.1	466	1	GIPR HUMAN
29	635.5	21.9	553	1	GLP2 HUMAN
30	630.5	21.7	423	1	GRFR HUMAN
31	628.5	21.6	463	1	GLP1 HUMAN
32	622.5	21.4	423	1	GRFR PIG
33	619	21.3	477	1	GLR_HUMAN

34	616	21.2	455	1	GIPR RAT	P43219 rattus norv
35	607	20.9	485	1	GLR RAT	P30082 rattus norv
36	596.5	20.5	423	1	GRFR MOUSE	P32082 mus musculu
37	595	20.5	485	1	GLR MOUSE	O61606 mus musculu
38	594.5	20.5	478	1	CALR_CAVPO	O08893 cavia porce
39	589.5	20.3	515	1	CALR_MOUSE	Q60755 mus musculu
40	581	20.0	516	1	CALR RAT	P32214 rattus norv
41	579.5	19.9	490	1	CALR HUMAN	P30988 homo sapien
42	576	19.8	474	1	CALR RABIT	P79222 oryctolagus
43	574	19.7	464	1	GRFR RAT	Q02644 rattus norv
44	554.5	19.1	420	1	CRF1_CHICK	Q90812 gallus gall
45	544.5	18.7	498	1	CALR_PIG	P25117 sus scrofa

ALIGNMENTS

RESULT 1

ID	PTH2_HUMAN	STANDARD;	PRT;	550 AA.
AC	P49190;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Parathyroid hormone receptor precursor (PTH2 receptor).			
GN	PTH2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.			
TX	TISSUE=Brain;			
RX	MEDLINE=95318121; PubMed=7797535;			
RA	Usdin T.B., Gruber C., Bonner T.I.;			
RT	"Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor.";			
RL	J. Biol. Chem. 270:15455-15458(1995).			
RN	[2]			
RP	SEQUENCE OF 26-40 AND 306-550 FROM N.A.			
RX	MEDLINE=97079671; PubMed=8921382;			
RA	Usdin T.B., Modi W., Bonner T.I.;			
RT	"Assignment of the human PTH2 receptor gene (PTH2) to chromosome 2q33 by fluorescence in situ hybridization.";			
RL	Genomics 37:140-141(1996).			
CC	ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL CYCLASE.			
CC	TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.			
CC	ALSO EXPRESSED IN THE TESTIS.			
CC	!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.			

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DR	EMBL; U25128; AAC50157.1; -	
DR	EMBL; U47124; AAA96796.1; -	
DR	EMBL; U47129; AAC50767.1; -	
DR	EMBL; U47125; AAC50767.1; JOINED.	
DR	EMBL; U47126; AAC50767.1; JOINED.	
DR	EMBL; U47127; AAC50767.1; JOINED.	
DR	EMBL; U47128; AAC50767.1; JOINED.	
DR	PIR; A57519; A57519.	
DR	Genew; HGNC:9609; PTHR2.	
DR	MIM; 601459; -	
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.	
DR	GO; GO:0004991; F:parathyroid hormone receptor activity; TAS.	
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin...; TAS.	


```

Db 144 RCDNSGSELVPGNRRWYANSECVKELTNETR--EREVDFRLGMIVTVGYSISLSGLTV 201
Qy 162 AILIGYFRRLHCTRNTHMHLFVSFMLRATSIKDRVVAHIGVKELESIMQDDPON 221
Db 202 AVILIGYFRRLHCTRNTHMHLFVSFMLRAVSIKDAVLSGYSTDEIER-ITEELRA 260
Qy 222 SIEATSDVKQYICKIAVMFIYFLATNYYWILVEGLYHLNLFVAFPSDTKYLMGFIL 281
Db 261 FTEPPADKAGFCVAVTVFLYFLATNYYWILVEGLYHLNLFVAFPSDTKYLMGFIL 320
Qy 282 IGMGFPAAFAVAARATLADARCELSAGDIKWIYQAPILAAIGLNFILFLNTVILA 341
Db 321 FGWGLPAVFAVAVTVFLATLANTECWDLSGKNKWIQVPIAAVNFILFINIIRVLA 380
Qy 342 TKIWTETNAVGHDTKQYKRLAKSLVILVFGVHYIVFVCLPHS-FTGLGWEIRHCELF 400
Db 381 TKLRETNAGRCDTRQYKRLKSLVILVPLFGVHYIVFMATPYTEVSGILMQVQHYEML 440
Qy 401 FNSPQGFVFIYCYCNGEVOAECVQKWSRNLSVDMKRTPPCGSRRCGSLVTTVTH-- 457
Db 441 FNSPQGFVFIYCYCNGEVOAECVQKWSRNLSVDMKRTPPCGSRRCGSLVTTVTH-- 493
Qy 458 -STSSQSOVAAHAWCLSLAKLPRSPADSLTATSLYLSAMSGVTSQTSRASHLSTRSKED 516
Db 494 VSHTSVTNVPGRGLALSLS--PRLAPGAGASANGHQLPGYVKHGSISEN-SLPSSGPE 550
Qy 517 SGRQDDILM-----EKSPRPMESNPT 539
Db 551 PGTKDDGLNGSLGYEPWVGQPPLEERET 583

RESULT 4
PTRR_PIG
ID PTRR_PIG STANDARD; PRT; 585 AA.
AC P50133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE precursor (PTH/PTHr receptor).
GN PTHr1 OR PTHr.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96305358; PubMed=8688470;
RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
RA Chandrasekhar S., Hsiung H.M.;
RT "Structure and functional expression of a complementary DNA for
RT porcine parathyroid hormone/parathyroid hormone-related peptide
RT receptor."
RL Biochim. Biophys. Acta 1307:339-347(1996).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATES ADENYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U18315; AAC48619.1; --
CC HSSP; Q03431; IBL1.

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DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm.2; 1.
DR PRINTS; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G PROTEIN RECP_F2_1; 1.
DR PROSITE; PS00650; G PROTEIN RECP_F2_2; 1.
DR PROSITE; PS00227; G PROTEIN RECP_F2_3; 1.
DR PROSITE; PS00261; G PROTEIN RECP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 27 585
FT DOMAIN 27 184
FT TRANSMEM 185 208
FT DOMAIN 209 215
FT TRANSMEM 216 235
FT DOMAIN 236 277
FT TRANSMEM 278 301
FT DOMAIN 302 315
FT TRANSMEM 316 337
FT DOMAIN 338 356
FT TRANSMEM 357 377
FT DOMAIN 378 404
FT TRANSMEM 405 423
FT DOMAIN 424 435
FT TRANSMEM 436 458
FT DOMAIN 459 585
FT DISULFID 48 113
FT DISULFID 104 144
FT DISULFID 127 166
FT CARBOHYD 147 147
FT CARBOHYD 157 157
FT CARBOHYD 162 162
FT CARBOHYD 172 172
SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;

Query Match 46.3%; Score 1345; DB 1; Length 585;
Best Local Similarity 52.5%; Pred. No. 2.2e-95;
Matches 259; Conservative 75; Mismatches 101; Indels 58; Gaps 7;

Qy 4 LGASLHVWGWLMLGSCLL---ARAQLDSDGTTITIEBQIVLVKAKVQCELNITAQIQ-- 57
Db 1 MGAARIAPGLALLCCPVLLSAVALVDADVMTKERQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 58 -----EGBGN-----CFPNDGLICWPRGTVG 79
Db 61 DIMESDKGWASAPTSKPKREKASGLYPESGSDTSGRHQGRPCLPFDHILCPLGAPG 120
Qy 80 KISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTNWANYSDCLRFLOPDISIGKOE 139
Db 121 EVVAMECPDIYDFNKHGHAIRCDRNGSWELVPGHNRWANYSECVKFLTNETR--ERE 178
Qy 140 FCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTHMHLFVSFMLRATSIKDR 199
Db 179 VFDELGMIVTVGYSVSLASLITVAVLILAYFRRLHCTRNTHMHLFVSFMLRAVSIK 238
Qy 200 VVHAHIGVKELESIMQD-----DPQNSIEATSDVKQYICKIAVMFIYFLATNYYW 253
Db 239 VLYSGATLDEAERLITEELRAIAQAFLPPVAATS-----YVGRVAVTFPLYFLATNYYW 293
Qy 254 ILVEGLYHLNLFVAFPSDTKYLMGFILGWGFPAAFAVAARATLADARCELSAGD 313
Db 294 ILVEGLYHLNLFVAFPSDTKYLMGFILGWGFPAAFAVAARATLADARCELSAGD 353
Qy 314 IKWYIQAFLAAIGLNFILFLNTVRLATKIETNAVGHDTKQYKRLAKSLTIVLVFG 373
Db 354 KKWIIQVILASIVLNFILFINIVRLATKLRETNAGRCDTQYKRLAKSLTIVLVFG 413
Qy 374 VHYIVFVCLPHS-FTGLGWEIRHCELFNSGQGFVSIYCYCNGEVOAECVQKWSRN 432
Db 414 VHYIVFVCLPHS-FTGLGWEIRHCELFNSGQGFVSIYCYCNGEVOAECVQKWSRN 473

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QY 433 LSVDWKRTPCGS 445
 Db 474 LALDFKRSQS 486

RESULT 5
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 AC Q03431;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE Precursor (PTH/PTHr receptor).
 GN PTHr1 OR PTHr.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93238641; PubMed=8386612;
 RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Juppner H.;
 RT "Identical complementary deoxyribonucleic acids encode a human renal
 RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
 RL Endocrinology 132:2157-2165(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93387403; PubMed=8397094;
 RA Schneider H., Feyen J.-H., Rao Movva N.;
 RT "Cloning and functional expression of a human parathyroid hormone
 RT receptor.";
 RL Eur. J. Pharmacol. 246:149-155(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95263723; PubMed=7745008;
 RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,
 RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtko J., Dop C.,
 RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Juppner H.;
 RT "Pseudohypoparathyroidism type 1b is not caused by mutations in the
 RT coding exons of the human parathyroid hormone (PTH)/PTH-related
 RT peptide receptor gene.";
 RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Levine M.A.;
 RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP EXTRACELLULAR DOMAIN DISULFIDE BONDS.
 RX MEDLINE=20374568; PubMed=10913300;
 RA Grauschopf U., Lilie H., Honold K., Wozny M., Reusch D., Esswein A.,
 RA Schafer W., Rucknagel K.P., Rudolph R.;
 RT "The N-terminal fragment of human parathyroid hormone receptor 1
 RT constitutes a hormone binding domain and reveals a distinct disulfide
 RT pattern.";
 RL Biochemistry 39:8878-8887(2000).
 RN [6]
 RP STRUCTURE BY NMR OF 168-198.
 RX MEDLINE=98409426; PubMed=9737850;
 RA Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;
 RT "Binding domain of human parathyroid hormone receptor: from
 RT conformation to function.";
 RL Biochemistry 37:12737-12743(1998).
 RN [7]
 RP VARIANT MURK-JANSEN ARG-223.
 RX MEDLINE=95215874; PubMed=7701349;
 RA Schipani E., Kruse K., Juppner H.;

RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type
 RT metaphyseal chondrodysplasia.";
 RL Science 268:98-100(1995).
 RN [8]
 RP VARIANTS MURK-JANSEN ARG-223 AND PRO-410.
 RX MEDLINE=96366745; PubMed=87031170;
 RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
 RA Kooh S.W., Cole W.G., Juppner H.;
 RT "Constitutively activated receptors for parathyroid hormone and
 RT parathyroid hormone-related peptide in Jansen's metaphyseal
 RT chondrodysplasia.";
 RL New Engl. J. Med. 335:708-714(1996).
 RN [9]
 RP MUTAGENESIS OF ARG-223 AND PRO-410.
 RX MEDLINE=97322091; PubMed=9178745;
 RA Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
 RA Juppner H.;
 RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
 RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
 RT receptors mutated at the two loci for Jansen's metaphyseal
 RT chondrodysplasia.";
 RL Mol. Endocrinol. 11:851-858(1997).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
 CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 CC SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN
 CC KIDNEY, BONE AND LIVER.
 CC -1- DISEASE: DEFECTS IN PTHr1 ARE THE CAUSE OF BLOWSTRAND TYPE OF
 CC CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA.
 CC -1- DISEASE: DEFECTS IN PTHr1 ARE THE CAUSE OF MURK-JANSEN TYPE OF
 CC METAPHYSEAL CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA. IT IS
 CC A RARE FORM OF SHORT-LIMBED DWARFISM ASSOCIATED WITH HYPERCALCEMIA
 CC AND NORMAL OR LOW SERUM CONCENTRATIONS OF THE TWO PARATHYROID
 CC HORMONES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL; L04308; AAA36525.1; -
 CC EMBL; X68596; CAA48589.1; -
 CC EMBL; U22409; AAB60657.1; -
 CC EMBL; U22401; AAB60657.1; JOINED.
 CC EMBL; U22402; AAB60657.1; JOINED.
 CC EMBL; U22403; AAB60657.1; JOINED.
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 CC EMBL; U22406; AAB60657.1; JOINED.
 CC EMBL; U22407; AAB60657.1; JOINED.
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 CC EMBL; U17418; AAA56774.1; -
 CC PIR; I38139; A49191
 CC PDB; 1BL1; 30-MAR-99.
 CC PDB; 1ET2; 06-SEP-00.
 CC PDB; 1ET3; 06-SEP-00.
 CC Genew; HGNC:9608; PTHr1.
 CC MIM; 168468; -
 CC MIM; 156400; -
 CC MIM; 215045; -
 CC GO; GO:0005737; Cytoplasm; TAS.
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0005634; C:nucleus; TAS.
 CC GO; GO:0004991; F:parathyroid hormone receptor activity; TAS.
 CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
 CC GO; GO:0001501; P:skeletal development; TAS.

[illegible]

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DR	InterPro; IPR001879; hormn_receptor.
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DR	Pfam; PF02793; HRM; 1.
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DR	SMART; SMO0008; HORMR; 1
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DR	PROSITE; PS00650; G_PROTEIN_REC_P2_2; 1.
DR	PROSITE; PS00227; G_PROTEIN_REC_P2_3; 1.
DR	PROSITE; PS00261; G_PROTEIN_REC_P2_4; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW	Disease mutation; 3D-structure; Dwarfism.
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FT	CHAIN 1 26
FT	FT CHAIN 27 593 PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR.
FT	DOMAIN 27 188 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 189 212 1 (POTENTIAL).
FT	DOMAIN 213 219 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 220 239 2 (POTENTIAL).
FT	DOMAIN 240 282 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 283 306 3 (POTENTIAL).
FT	DOMAIN 307 320 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 321 342 4 (POTENTIAL).
FT	DOMAIN 343 361 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 362 382 5 (POTENTIAL).
FT	DOMAIN 383 409 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 410 428 6 (POTENTIAL).
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FT	DOMAIN 464 593 CYTOPLASMIC (POTENTIAL).
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FT	DISULFID 131 170
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FT	CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT	CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARIANT 223 223 H -> R (IN MURK JANSSEN; CONSTITUTIVELY ACTIVATED).
FT	FT FT /FTIG=VAR 003582.
FT	FT VARIANT 410 410 T -> P (IN MURK JANSSEN; CONSTITUTIVELY ACTIVATED).
FT	FT FT /FTIG=VAR 003583.
FT	CONFLICT 471 471 K -> N (IN REF. 2).
FT	CONFLICT 473 473 S -> C (IN REF. 2).
FT	HELIX 169 176
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Db	Best Local Similarity 47.4%; Pred. No. 9.7e-95;
Db	Matches 276; Conservative 81; Mismatches 134; Indels 91; Gaps 11;
QY	22 ARAQLDSGDTTIEBQILVLVKAKVQCRLNITAQLQ----- 57
Db	22 AVALVDADVMTKEEQIFLLHRAQQCKRKLEVLQRPASTMESDKGTWSASTSGKPKRD 81
QY	58 -----EGEGN-----CPPEWDGLICWRPGTVGVKISAVPCPPPIYDFNHK 96
Db	82 KASGKLYPESEDEKEAPTSRGVRGPCLPENDHILCWPLGAPGEVAVPCDIYDFNHK 141
QY	97 GVAFRCNPNGTWDMHSLNKTWANYSDCLRFQFDISIGKQFCERLYMYTVGVYSISF 156
Db	142 GHAYRCDRNGSWELVPQHNRITWANYSECVFLETNETR--EREVFDRLGLMIYTVGVSVL 199
QY	157 GSILAVALIIGYFRFLHCTRNVIHMLFPVSFMLRATSFVKVDKVVAHIHVKELESJ--- 213
Db	200 ASLTAVAILAYFRHLCTRNVIHMLFSLFMRKAVSLFVKDAVLYSGATLDEAERTEE 259
QY	214 ----IMQDDPNQSIEATSVDKSQYIGCKIAVMFIPLATNYWILVEGLYLHNLIFFAV 269
Db	260 ELURAQAAPPPTAAAG----YAGCRVAVTFEFLFYLATNYWILVEGLYLHSLFMFAF 314

or send an email to license@isb-sib.ch).

	or send an email to license@isb-sib.ch).						
CC							
CC	-----						
DR	EMBL; M77184; AAA41811.1;	--					
DR	EMBL; L19475; AAA68098.1;	--					
DR	PTR; I54195; I54195.						
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DR	InterPro; IPRO00832; GPCR_secretin.						
DR	InterPro; IPRO01879; hormn_receptor.						
DR	Pfam; PF00002; 7tm_2; 1.						
DR	Pfam; PF02793; HRM; 1.						
DR	PRINTS; PR00249; GPCRCRETIN.						
DR	SMART; SMO0008; Hormr; 1.						
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FT	DOMAIN	27	188	EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM	189	212	1 (POTENTIAL).			
FT	DOMAIN	213	219	CYTOLASMIC (POTENTIAL).			
FT	TRANSMEM	220	239	2 (POTENTIAL).			
FT	DOMAIN	240	282	EXTRACELLULAR (POTENTIAL).			
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FT	TRANSMEM	410	428	6 (POTENTIAL).			
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QY	97 GVAFRHCPNGTWDPMHSINKNTWANYSCLFLQPDTSIGKQECERLYVMYTVGYVSISF	156					
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QY	157 GSIAVALIIGTFRELHLCTRNYHMHLFSVSMELRATSIFVKDRVVAHHIGHVKELES---	213					
Db	200 ASLTVAVALIAYFREHLCHTRNYIHMMFLSPMLRAASI FVKDAVLYSGFTLD EAERLTEE	259					
QY	214 ----IMQDDPONSI EATSVDSKYIGCKIAVMFIYFLATNYWILVEGLYLHNLFVAP	269					
Db	260 ELHIHQVPPPAAAAVG-----YAGCRVAVTFIFYLATNYWILVEGLYLHSLFMFAF	314					
QY	270 FSDTKYLGMGFI LGWGFPA A VAAWA VARATLA DARCWELS AGDKIWIOCAPILAIGN	329					
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Db 375 FILFNIIIRVLATKLRETNAGRCDFEQVKLLRSTLVLPVFGVHYTVFMALPYEVS 431
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Db 435 TLWQIOMHYEMLFNSFOFFVIAIYFCNGEVOAEIRKSWRSWTLLDLPFKRARGSS 494
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QY 502 KTASHTLSTRS-----NKEDSGRQRDDILMEX 528
Db 547 ETLPTVMAVPKDDGFLNGSCGLDDEASGSARPPPLQOE 585

RESULT 7
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AC P41593; Q62119;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE precursor (PTHrP/PTHr receptor).
GN PTHR1 OR PTHR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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RC STRAIN=C3H/HEHA;
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RA Karperien M., van Dijk T.B., Hoeijmakers T., Cremers F.,
RA Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
RT "Expression pattern of parathyroid hormone/parathyroid hormone
RT related peptide receptor mRNA in mouse postimplantation embryos
RT indicates involvement in multiple developmental processes.";
RL Mech. Dev. 47:29-42(1994).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94255468; PubMed=8197183;
RA McCuaig K.A., Clarke J.C., White J.H.;
RT "Molecular cloning of the gene encoding the mouse parathyroid
RT hormone/parathyroid hormone-related peptide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; X78936; CAA55536.1; --
CC EMBL; L34611; AAA40011.1; --
CC EMBL; L34608; AAA40011.1; JOINED.
CC EMBL; L34607; AAA40011.1; JOINED.
CC EMBL; L34609; AAA40011.1; JOINED.
CC EMBL; L34610; AAA40011.1; JOINED.
CC PIR; I59297; I59297.
CC DR PIR; S44203; S44203.
CC DR HSSP; Q03431; IRL1.

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 GO; GO:0001501; P:skeletal development; IMP.
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 SMART; SMO0008; Hormr; 1.
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 PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
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 G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
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 CARBOHYD 176 176
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 CONFLICT 500 501
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 22 AVALVDADDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAANIMESDKGWTFASTSGKPKKE 81
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 260 ELHIIAQVPPPPAAAAVG-----YAGCRVAVTFYFLATNYIWLVEGLYHLNLIFFAVF 314
 270 FSDTKYLGWFGILGWGFPFAAFVAWAVARATLADARCWELSGADIKWIVQAPILAAIGLN 329
 315 FSEKYLWGFTIFGWLGPFAVFAVWVGVVRATLANTGCDLSSGKKHIIQVPIASVVLN 374
 330 FILFLNTVRVLATKIWTETNAVGHDRKQVRKLAKSTLVLLVLFVGVHYYIVFVCLPHS-FTG 388

Db 375 FILFINIIRVLATKIRETNAGRCDTQKQYKLESLTLVPLFGVHYTFVMAIPYTEVSG 434
 Qy 389 LGWEIRMHCELFNSFGQFFVSIYVCNCEVQAEVKKMWSRWNLSDVWKERTPPCGS 445
 Db 435 TLWQIQWHEYMLFNSFGQFFVSIYFCNCEVQAEIRKSWRSWTALDLDFKKARSGS 491
 RESULT 8
 SCRC RAT
 ID SCRC RAT STANDARD; PRT; 449 AA.
 AC P2381;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Secretin receptor precursor (SCT-R).
 GN SCTR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91266890; PubMed=1646711;
 RA Ishihara T., Nakamura S., Kaziro Y., Takahashi T., Takahashi K.,
 RA Nagata S.;
 RT "Molecular cloning and expression of a cDNA encoding the secretin
 RT receptor.";
 RL EMBO J. 10:1635-1641(1991).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CC CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X59132; CAA41849.1; -
 CC F1R; S16319; S16319.
 CC InterPro; IPR000832; GPCR secretin.
 CC InterPro; IPR001879; hormn_receptor.
 CC Pfam; PF00002; 7tm2; 1.
 CC Pfam; PF02793; HRM; 1.
 CC PRINTS; PR00249; GPCRSSECRETIN.
 CC SMART; SMO0008; Hormr; 1.
 CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 CC PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 CC PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 CC SIGNAL 1 22
 CC CHAIN 23 449
 CC SECRETIN RECEPTOR.
 CC DOMAIN 23 143
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSSEM 144 167
 CC DOMAIN 168 174
 CC TRANSSEM 175 194
 CC DOMAIN 195 216
 CC TRANSSEM 217 240
 CC DOMAIN 241 254
 CC TRANSSEM 255 276
 CC DOMAIN 277 294
 CC TRANSSEM 295 317
 CC DOMAIN 318 343
 CC TRANSSEM 344 362
 CC DOMAIN 363 369
 CC TRANSSEM 370 392
 CC DOMAIN 393 449
 CC CYTOPLASMIC (POTENTIAL).


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FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 449 AA; 51234 MW; E70D05B5D061480D CRC64;

Query Match 27.6%; Score 801; DB 1; Length 449;
Best Local Similarity 37.3%; Pred. No. 6e-54;
Matches 176; Conservative 81; Mismatches 149; Indels 66; Gaps 15;

QY 14 LMLGSCLLARALQSDSGTITIEBQIVLVKAKVQCELNITAQL-OBEGNCPE----- 66
DQ LLLRLLLTKAA-----HTGVPRPLCDVRVLLEBAHCLQLSKKALGEPETASGCE 67
QY 67 --WDGLICWPRGTGKISAVPCPPYIDF-NHKGVAPRHCNPNGTWDFMH 113
DQ 68 GLWDMNSCWSPSAPARTVEVQCPKFLMLSNKNGSLFRNCTQDG-----WSE-- 114
QY 124 DCLRFLOPDISG---KQEFCEP-----LVVMYTVGYSISFGSLAVAILIIGYFRLH 173
DQ 115 ---TFPRDLACGVNINNFERRHAYLLKLMYTVGYSSSLAMLLVALSLCFSRRLH 171
QY 174 CTRNYHMLFVSFMLRATSFVKDORVVAHIGVKELESIMQDDPQNSIEATSDKSOY 233
DQ 172 CTRNYHMLFVSFILRALSFIKDAV-----LFSSDD-----VTYCD-AHK 212
QY 234 IOCKIAVVMFIYFLANNYIWLVEGLYHNLIFVAFPSDTKYLWGLFGLGWGFPAAVAA 293
DQ 213 VGCKLVMIFFQYICIMANYAMVLLVEGLYHNLIFVAFPSDTKYLWGLFGLGWGFPAAV 272
QY 294 MAVARATLADARCWELSA-GDKIKYQAPILAAIGNLFILNTVRLATKIWETNAVGH 352
DQ 273 WAITHRELFENTGCWDINANASVWVIRGVPVLSILNFIFFNIIIRLMKRLTOETRGS 332
QY 353 DTRKYRKLAKSTLVLVFVGHYIVFVCLPHSFGLGWEIRMCHELFNSFGQFVSII 412
DQ 333 ET-NHYKRLAKSTLLILPLFGHYIVAFSPED-----AMEVQLFELALGSGQGLVAVL 387
QY 413 YCYCNCEGVOAEYKQWMSRNLSDVKRTPPCGSRRCGSLVLTVTHTSSQSQ 464
DQ 388 YCFLNGEVOLEQKQKRWHLQ-EPLRLPVAFNNSFNATNGPTHTSKASTE 438

RESULT 9
SCRC RABIT
ID SCRC RABIT STANDARD; PRT; 445 AA.
AC O46502;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Secretin receptor precursor (SCT-R).
GN SCTR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_taxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98366112; PubMed=9700755;
RA Svoboda M., Tastenoy M., de Neef P., Delpoite C., Waelbroeck M.,
RA "Robrecht P.;
RT "Molecular cloning and in vitro properties of the recombinant rabbit
RT secretin receptor."
RL Peptides 19:1055-1062 (1998).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; AF025411; AAC32767.1; --
 DR InterPro; IPR000832; GPCR_Secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HormR; 1.
 DR PROSITE; PS00849; G-PROTEIN RECP_F2_1; 1.
 DR PROSITE; PS00650; G-PROTEIN RECP_F2_2; 1.
 DR PROSITE; PS00227; G-PROTEIN RECP_F2_3; 1.
 DR PROSITE; PS00261; G-PROTEIN RECP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 445
 FT DOMAIN 22 139
 FT TRANSMEM 140 163
 FT DOMAIN 164 170
 FT TRANSMEM 171 190
 FT DOMAIN 191 212
 FT TRANSMEM 213 236
 FT DOMAIN 237 250
 FT TRANSMEM 251 272
 FT DOMAIN 273 290
 FT TRANSMEM 291 313
 FT DOMAIN 314 339
 FT TRANSMEM 340 358
 FT DOMAIN 359 365
 FT TRANSMEM 366 388
 FT DOMAIN 389 445
 FT CARBOHYD 68 68
 FT CARBOHYD 96 96
 FT CARBOHYD 102 102
 FT CARBOHYD 124 124
 SQ SEQUENCE 445 AA; 50495 MW; 31C4169CB099F194 CRC64;

Query Match 27.3%; Score 794; DB 1; Length 445;
 Best Local Similarity 37.4%; Pred. No. 2e-53;

Matches 182; Conservative 71; Mismatches 135; Indels 98; Gaps 17;

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QY 13 WMLGSCLLARALQSDSGTITIEBQIVLVKAKVQCELNITAQL-OBEGNCPE----- 66
DQ 12 WLLGFACAAH-----LVGAPRLCD--VLWVLOEERDQCLQELERERL 53
QY 67 -----WDGLICWPRGTGKISAVPCPPYIDF-NHKGVAPRHCNPNGTWDFMH 113
DQ 54 GEEQVPQCQGLWDMNSCWSPSAPGRVVELCPRFLMLTNSGSLFRNCTQDG----- 107
QY 114 SLNKTWANSCLRFLOPDISG-----KQEFCELYVMYTVGYSISFGSLAVAI 163
DQ 108 -----WTE-----TFPRDLACGVNINNFERRHAYLLKLMYTVGYSSSLAMLLVAL 157
QY 164 LIIGYFRLHCTRYNIHMLFVSFMLRATSFVKDORVVAHIGVKELESIMQDDPQNSI 223
DQ 158 GILCAFRLLHCTRYNIHMLFVSFMLRATSFVKDORVVAHIGVKELESIMQDDPQNSI 200
QY 224 EATSVDSQYICKIAVVMFIYFLANNYIWLVEGLYHNLIFVAFPSDTKYLWGLFGLGW 283
DQ 201 -AIHCD-AHRVGCKLVVFFQYICIMANYAMVLLVEGLYHNLIFVAFPSDTKYLWGLFGLGW 258
QY 284 WGFPAFVAWAVARATLADARCWELSA-GDKIKYQAPILAAIGNLFILNTVRLAT 342
DQ 259 WGSFAMFVTSMAVTRHFLSDSGCWDINANAAIWWIRGVPVLSILNFIINILRILTR 318
QY 343 KIWETNAVGHCTRYNIHMLFVSFMLRATSFVKDORVVAHIGVKELESIMQDDPQNSI 402
DQ 319 KLRTQETRGQD-MNHYKRLAKSTLLILPLFGHYIVAFSPED-----AMBIQLFFELALG 373

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OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=99265976; PubMed=10331949;
 RA Hashimoto H., Nishino A., Shintani N., Hagiwara N., Copeland N.G.,
 RA Jenkins N.A., Yamamoto K., Matsuda T., Ishihara T., Nagata S.,
 RA Baba A.;
 RT "Genomic organization and chromosomal location of the mouse vasoactive
 intestinal polypeptide 1 (VIP1) receptor.";
 RL Genomics 58:190-93(1999).
 RN [2]
 RP SEQUENCE OF 249-398 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Thymus;
 RX MEDLINE=96378704; PubMed=8784267;
 RA Johnson M.C., McCormack R.J., Delgado M., Martinez C., Ganea D.;
 RT "Murine T-lymphocytes express vasoactive intestinal peptide receptor
 1 (VIP-R1) mRNA.";
 RL J. Neuroimmunol. 68:109-119(1996).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
 RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 DR EMBL; AB022860; BAA81896.1; JOINED.
 DR EMBL; AB022848; BAA81896.1; JOINED.
 DR EMBL; AB022849; BAA81896.1; JOINED.
 DR EMBL; AB022850; BAA81896.1; JOINED.
 DR EMBL; AB022851; BAA81896.1; JOINED.
 DR EMBL; AB022852; BAA81896.1; JOINED.
 DR EMBL; AB022853; BAA81896.1; JOINED.
 DR EMBL; AB022854; BAA81896.1; JOINED.
 DR EMBL; AB022855; BAA81896.1; JOINED.
 DR EMBL; AB022856; BAA81896.1; JOINED.
 DR EMBL; AB022857; BAA81896.1; JOINED.
 DR EMBL; AB022858; BAA81896.1; JOINED.
 DR EMBL; AB022859; BAA81896.1; JOINED.
 DR EMBL; S82970; AAN86759.1; JOINED.
 DR MGD; MGI:109272; Vipr1.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HORMR; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 459 VASOACTIVE INTESTINAL POLYPEPTIDE
 RECEPTOR 1.
 FT DOMAIN 31 143
 FT TRANSMEM 144 168
 FT DOMAIN 169 175
 FT TRANSMEM 176 195
 FT DOMAIN 196 217
 FT TRANSMEM 218 241
 FT DOMAIN 242 255
 FT TRANSMEM 256 277
 FT DOMAIN 31 143
 FT TRANSMEM 144 168
 FT DOMAIN 169 175
 FT TRANSMEM 176 195
 FT DOMAIN 196 217
 FT TRANSMEM 218 241
 FT DOMAIN 242 255
 FT TRANSMEM 256 277

FT DOMAIN 278 294
 FT TRANSMEM 295 318
 FT DOMAIN 319 343
 FT TRANSMEM 344 363
 FT DOMAIN 364 375
 FT TRANSMEM 376 395
 FT DOMAIN 396 459
 FT DISULFID 216 286
 FT CARBOHYD 58 58
 FT CARBOHYD 69 69
 FT CARBOHYD 100 100
 FT CARBOHYD 104 104
 FT CARBOHYD 292 292
 SQ SEQUENCE 459 AA; 52094 MW; CQC3A9AE1ADF61ID CRC64;
 Query Match 27.2%; Score 791.5; DB 1; Length 459;
 Best Local Similarity 36.6%; Pred. No. 3.3e-53;
 Matches 181; Conservative 81; Mismatches 145; Indels 87; Gaps 19;
 QY 13 WLMGSCLLARA---QLDSGTITIE-----EQVLVLKAKVQCELNITLQLEGEGNCF 64
 DB 11 WL-----CVLAGALACALGPAGSRAASPHQCEYLQMIKQKQCCLE--AQLENKTTGCS 64
 QY 65 PEWDGLICWPRGTGKISAVPCPEYIYDFN--HKGVAFRHCNPNGTWDFVHSLNKTWANY 122
 DB 65 KMDNLTCTWPTTPWGQVVVLDCLIFOLFSPHIGYNISRNCTEG-----WSQ- 112
 QY 123 SDCLRFLOP---DISIG-----KQPCERLYVMYTVGYISFGSLAVAILIG 167
 DB 113 -----LEPGPYHACGLINDRASSMDQOQTEFYDAVKTYGTIGYSLSLASLLVAMAILS 166
 QY 168 YFRLLHCTRNVIHMHFLVFSWMLRATSFVDRVVAHIGVKELESILMQDDPQNSIATS 227
 DB 167 LFRKLHCTRNVIHMHFLVFSWMLRATSFVDRVVAHIGVKELESILMQDDPQNSIATS 227
 QY 228 VDKSQYIGCKIAYVMFYIATNYIWLVEGLYHNLIFVAFPSDTKYLWGLFILIGWFP 287
 DB 214 -----VSKAAVVFQYCYMANFFLLVGLYHNLIFVAFPSDTKYLWGLFILIGWFP 287
 QY 288 AAFVAAVAVATLADARCE--LSAGDKIYQAPILAAIGLNFILFNTVRVLATKIWE 346
 DB 268 SVFIMWTIVRIHFEDFGCWDTIINSSLMWIKGPIISILVNFILFICIRILVQLR 327
 QY 347 TNAVGHDRKQYKRLAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMECELFNFSQ 406
 DB 328 PD-IGKNDSSPSYSLAKSTLLILFLFGVHYVMAFFDNFKA---QVAMFELVVGSG 383
 QY 407 FVSIITYCNGEVOAEVKKMSRWNLNLS--VDW--KTPFCGSR--CG---SVLTFTV 456
 DB 384 FVVAIYCFNGEVOAELRKRRWHLQGVLGWSKSHQHPWGGSGNGVSCSTQVSMLTRVS 443
 QY 457 ---HSTSSQSOVA 466
 DB 444 PSARRSSSFQAEVS 457
 RESULT 12
 ID VIPR_PIG STANDARD; PRT; 458 AA.
 AC Q28992;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1)
 DE (Pituitary adenylate cyclase activating polypeptide type II receptor)
 DE (PACAP type II receptor) (PACAP-R-2).
 GN VIPR1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.

Db 194 FIKDMALF-----NSGEIDHCSEAS-VGCKAAVVFQYCVMANFFWL 234
QY 255 LVEGLYLHNLIFVAFPSDTKYLWGFFILICWGFPAAAFVAAWAVARATLADARCWE-LSAGD 313
Db 235 LVEGLYLYTLAVSFSEKYPWGYLILCWGVPVFIITWTVRYFFEDFGCWDTIINSS 294
QY 314 IKWIYQAPILAAIGLNFILFNLTVRVLATKIWETNAVGHDTKQYRKLAKSTLVLVLVPG 373
Db 295 LWWIIKAPILLSILNVNLFICIIRILVQKLPPD-IGKNDSSPYSLAKSTLLIPLFG 353
QY 374 VHVIVFVCLPHSFTGLGWEIRMHCELFNFSFGFFVUSIICYCNGEVOAEVKKWNRNL 433
Db 354 IHVMPAFPPDNFKA---QVKWVFEVLVGSFGFVVAILYCFNGEVOAELERRKWRNHL 410
QY 434 S--VDW--KRTPECGSRR---CG---SVLTTVT---HSTSSQSOVA 466
Db 411 QGVLGWSSKSQHFWGSGNGATCSTQVSMLTRVSPSARRSSSFQAEVS 457

Search completed: November 21, 2003, 22:26:31
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 22:23:44 ; Search time 39 Seconds

(without alignments)
3579.653 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 2907

Sequence: 1 MAWLGLSLHWGMLGLSCL.....DDLMEKPRPMSNPDTREG 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.23:*
1: sp archaea.*
2: sp bacteria.*
3: sp fungi.*
4: sp human.*
5: sp invertebrate.*
6: sp mammal.*
7: sp mhc.*
8: sp organelle.*
9: sp phage.*
10: sp plant.*
11: sp rodent.*
12: sp virus.*
13: sp vertebrate.*
14: sp unclassified.*
15: sp rvirus.*
16: sp bacterioph.*
17: sp archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2635	90.6	621	4	Q8N429
2	2251.5	77.5	546	11	Q91V95
3	1677.5	57.7	575	13	Q9PWB7
4	1418.5	48.8	536	13	Q9PVD3
5	1345.5	46.3	595	6	Q9TU31
6	1324.5	45.6	591	11	Q91WV4
7	1307.5	45.0	542	13	Q9PVD2
8	962.5	33.1	964	4	Q8NHB4
9	858.5	29.5	169	11	Q9R1D4
10	814	28.0	444	13	Q9YHC6
11	803.5	27.6	237	11	Q8BUN8
12	794	27.3	419	13	Q8AXV3
13	791.5	27.2	459	11	Q9J140
14	787	27.1	419	13	Q8AXV4
15	783	26.9	528	4	Q81V17
16	780.5	26.8	333	4	Q8N5V1

17	780.5	26.8	418	13	Q9IBG2
18	771.3	24.5	465	13	Q73769
19	708.5	24.4	455	13	Q90Y10
20	702.5	24.2	438	13	Q73768
21	694	23.9	480	13	Q90Y07
22	692.5	23.8	459	11	Q8BGA4
23	685.5	23.6	465	13	Q9PTK1
24	685.5	23.6	495	13	Q90Y08
25	672.5	23.1	496	11	Q8BLT3
26	657.5	22.6	438	13	Q8AXV2
27	645.5	22.2	465	13	Q90Y09
28	645	22.2	489	13	Q8UYV4
29	644	22.2	490	13	Q8UYV5
30	636	21.9	423	6	Q9N1F8
31	635	21.8	423	6	Q9BDH9
32	633	21.8	441	6	Q9TUJ0
33	616	21.2	407	6	Q9BDI0
34	610	21.0	404	6	Q9TUJ1
35	604	20.8	439	11	Q9WU99
36	594	20.4	478	11	Q924D5
37	594	20.4	495	11	Q924D6
38	593	20.4	485	11	Q8K0B5
39	592	20.4	492	13	Q9PUK1
40	589.5	20.3	532	11	Q924D7
41	589	20.3	533	11	Q8CAB0
42	582	20.0	374	6	Q8WWR0
43	567	19.5	402	6	Q8WMO9
44	566.5	19.5	589	6	Q9GMD1
45	557	19.2	414	13	Q8AWA1

ALIGNMENTS

RESULT 1

Q8N429	Q8N429	PRELIMINARY;	PRT;	621 AA.
AC	Q8N429;			
DT	01-OCT-2002 (Tremblrel. 22, Created)			
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)			
DE	Parathyroid hormone receptor 2 (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Strausberg R.;			
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC036811; AAH36811.1; -			
DR	InterPro; IPR000832; GPCR_secretin.			
DR	InterPro; IPR001879; hormn_receptor.			
DR	Pfam; PF00002; 7tm_2; 1.			
DR	Pfam; PF02793; HRM; 1.			
DR	PRINTS; PR00249; GPCRSECRETIN.			
DR	SMART; SM00008; Hormr; 1.			
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.			
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.			
DR	PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.			
DR	PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.			
KW	Receptor.			
FT	NON TER			
SQ	SEQUENCE 621 AA; 69299 MW; 8B0A5A84898436D2 CRC64;			

Query Match 90.6%; Score 2635; DB 4; Length 621;
Best Local Similarity 91.4%; Pred. No. 1.6e-234;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

QY	1	MAWLGLSLHWGMLGLSCL	ARQLSDGPTTIEQIVLVKAKVQCELNITLQLOGE	60
DB	72	MAGLGLSLHWGMLGLSCL	ARQLSDGPTTIEQIVLVKAKVQCELNITLQLOGE	131


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QY 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 120
Db 132 GNCFFPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 191
QY 121 NYSDCRLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
Db 192 NYSDCRLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 251
QY 181 MHLFVSFMLRATSIKQFVORVVAHIGVKELESIMQDDPONSIEATSVDSKQYIGCKIAV 240
Db 252 MHLFVSFMLRATSIKQFVORVVAHIGVKELESIMQDDPONSIEATSVDSKQYIGCKIAV 311
QY 241 VMFIYFLATNYWILVEGLYHNLIIFVAFESDPTKYLWGFLIIGWGPFAAFVAWAVARAT 300
Db 312 VMFIYFLATNYWILVEGLYHNLIIFVAFESDPTKYLWGFLIIGWGPFAAFVAWAVARAT 371
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
Db 372 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 431
QY 361 LAKSTLVILVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNFSFGQFFVSIYCYCNGEV 420
Db 432 LAKSTLVILVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNFSFGQFFVSIYCYCNGEV 491
QY 421 QAEVKQWNRWNLSDWKRTPPCGSRRCGSLVLTVTHTSTSSQSOVAHAHAWCL---SLAK 477
Db 492 QAEVKQWNRWNLSDWKRTPPCGSRRCGSLVLTVTHTSTSSQSOVAHAHAWCL---SLAK 551
QY 478 LPRSPADSIATSLYLSMGSVTOQSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
Db 552 IASROPDS-----HITLPGYWSNSEQDCLPHSFHEETKEDSGRQDDILMEKPSRPME 605
QY 535 SNPDTEG 541
Db 606 SNPDTEG 612

RESULT 2
Q91V95 ID Q91V95 PRELIMINARY; PRT; 546 AA.
AC Q91V95;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Parathyroid hormone receptor.
GN PTHR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS, and ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-Throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354583; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF332078; AAK56106.1; --
DR EMBL; AF332077; AAK56105.1; --
DR EMBL; AK045576; BAC32420.1; --
DR MGD; MGI:2180917; Pthr2.
DR InterPro; IPR000832; GPCR_secretin.

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DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00293; HRM; 1.
DR SMART; SM00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
DR Receptor.
SQ SEQUENCE 546 AA; 61908 MW; 628051EF181A1DF3 CRC64;

Query Match 77.5%; Score 2251.5; DB 11; Length 546;
Best Local Similarity 78.3%; Pred. No. 3.4e-199;
Matches 426; Conservative 34; Mismatches 75; Indels 9; Gaps 4;

QY 1 MAWLKASLWGMWMLGSLCLLARAQLDSGTTTIEBQIVLVILKAKVQCCLNITAOLOEGE 60
Db 1 MAWLKASLWGMWMLGSLCLLARAQLDSGTTTIEBQIVLVILKAKVQCCLNITAOLOEGE 60
QY 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 120
Db 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 120
QY 121 NYSDCRLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
Db 121 NYSDCRLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
QY 181 MHLFVSFMLRATSIKQFVORVVAHIGVKELESIMQDDPONSIEATSVDSKQYIGCKIAV 240
Db 181 MHLFVSFMLRATSIKQFVORVVAHIGVKELESIMQDDPONSIEATSVDSKQYIGCKIAV 240
QY 179 LHLFVSFMLRATSIKQFVORVVAHIGVKELESIMQDDPONSIEATSVDSKQYIGCKIAV 238
Db 179 LHLFVSFMLRATSIKQFVORVVAHIGVKELESIMQDDPONSIEATSVDSKQYIGCKIAV 238
QY 241 VMFIYFLATNYWILVEGLYHNLIIFVAFESDPTKYLWGFLIIGWGPFAAFVAWAVARAT 300
Db 241 VMFIYFLATNYWILVEGLYHNLIIFVAFESDPTKYLWGFLIIGWGPFAAFVAWAVARAT 300
QY 239 VMFIYFLATNYWILVEGLYHNLIIFVAFESDPTKYLWGFLIIGWGPFAAFVAWAVARAT 298
Db 239 VMFIYFLATNYWILVEGLYHNLIIFVAFESDPTKYLWGFLIIGWGPFAAFVAWAVARAT 298
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
QY 299 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 357
Db 299 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 357
QY 361 LAKSTLVILVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNFSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVILVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNFSFGQFFVSIYCYCNGEV 420
QY 358 LAKSTLVILVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNFSFGQFFVSIYCYCNGEV 417
Db 358 LAKSTLVILVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNFSFGQFFVSIYCYCNGEV 417
QY 421 QAEVKQWNRWNLSDWKRTPPCGSRRCGSLVLTVTHTSTSSQSOVAHAHAWCLSLAKLPR 480
Db 421 QAEVKQWNRWNLSDWKRTPPCGSRRCGSLVLTVTHTSTSSQSOVAHAHAWCLSLAKLPR 480
QY 418 QAEVKQWNRWNLSDWKRTPPCGSRRCGSLVLTVTHTSTSSQSOVAHAHAWCLSLAKLPR 477
Db 418 QAEVKQWNRWNLSDWKRTPPCGSRRCGSLVLTVTHTSTSSQSOVAHAHAWCLSLAKLPR 477
QY 481 SPA---DSLITATSLYLSMGSVTOQSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 537
Db 481 SPA---DSLITATSLYLSMGSVTOQSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 537
QY 478 NACRQIDSHVTLPGYWSNSEQDCLPHSFHEETKEDSGRQDDILMEKPSRPME 534
Db 478 NACRQIDSHVTLPGYWSNSEQDCLPHSFHEETKEDSGRQDDILMEKPSRPME 534
QY 538 DTEG 541
Db 538 DTEG 538

RESULT 3
Q9PWB7 ID Q9PWB7 PRELIMINARY; PRT; 575 AA.
AC Q9PWB7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Parathyroid hormone type-2 receptor.
GN PTHR2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;

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RESULT 5	
Q9TU31	
ID Q9TU31	PRELIMINARY; PRT; 595 AA.
AC Q9TU31;	
DT 01-MAY-2000	(TRENBLrel. 13, Created)
DT 01-MAY-2000	(TRENBLrel. 13, last sequence update)
DT 01-OCT-2001	(TRENBLrel. 18, last annotation update)
DE	Parathyroid hormone receptor-1.

10	Q9PVD3	PRELIMINARY; FRU; 536 AA.
11	AC	
12	Q9PVD3	
13	01-MAY-2000	(TEMBLrel. 13, Created)
14	DT	01-MAY-2000 (TEMBLrel. 13, Last sequence update)
15	DT	01-MAY-2000 (TEMBLrel. 13, Last sequence update)
16	DT	01-OCT-2002 (TEMBLrel. 22, Last annotation update)
17	DE	Parathyroid hormone receptor PTHR.
18	GN	PTHRI.
19	OS	Brachydanio rerio (Zebrafish) (Danio rerio).
20	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
21	OC	

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GN PTH1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
CN NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
RT "Molecular cloning and functional characterization of the canine
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167095; AAD55938.1; -.
DR HSSP; Q03431; 1BL1.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7cm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 595 AA; 66308 MW; 09568ECF38D4D258 CRC64;

Query Match 46.3%; Score 1345.5; DB 6; Length 595;
Best Local Similarity 46.5%; Pred. No. 1.8e-115;
Matches 281; Conservative 90; Mismatches 154; Indels 79; Gaps 11;

QY 4 LGASLHWGWMIMLSGL--ARRQLSDGTITIEQIVLVKAKVQCEINITAIQ--- 57
DB 1 MGAVRIAPGLALLCCPVLSAYALVADDDVMTKEEQIFLLHRAQAQCKRLKEVLQRA 60
QY 58 -----EEGHN-----CFPEWDLICWPR 75
DB 61 DIMESDKWASASTSGPKKKEKASGLYPSEEDKEVPTGSRGRGRCLEPWHILCWPL 120
QY 76 GTVGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTNWYSDCLRFLOPDISI 135
DB 121 GAGEVVAVPCPDYIDFNHKGHAYRCDRNGSWELVPCHNRTWANYSECVKELTNETR- 179
QY 136 GKQFCERLYVWYTVGYSISGSLAVALLIGYFRRLHCTRNYYHMLFVSPMLRATSI 195
DB 180 -EREVFDRLGMIYTVGVSVSLASTVAVILAYFRRLHCTRNYYHMLFVSPMLRAVSI 238
QY 196 VKDRVWVAHIGVKELES!-----IMQDDPQNSIEATSDKSOYIGCKIAVWVFYFLA 248
DB 239 VKDAVLSGATLDEARLTERELALIAQAPPPPTAAA-----GYACRVAVTFFLYFLA 292
QY 249 TNYTWILVEGLYLNHLIFVAFPSDTKYLWGLFILGWGFPAAFVAWAVARATLADARWE 308
DB 293 TNYTWILVEGLYLNHLIFVAFPSDTKYLWGLFILGWGFPAAFVAWAVARATLADARWE 352
QY 309 LSAGDIKIYQAPILAAIGLNFILPLNTVRVLAETKIETNAVGHDTKQYRKLAKSTLVL 368
DB 353 LSSGNKWIIOQPIIASILVNFILFINVRVLAETKIETNAVGHDTKQYRKLAKSTLVL 412
QY 369 VLVFVGHVIVFVCLPHS--FTGLGWIRMHCELFNSFGGFVSIYCYCNAGEVQAEVKKM 427
DB 413 MFLFGVHIVFMATPYTEVSGTLVQVQVHYEMLFNSFGGFVSIYCYCNAGEVQAEIKKS 472
QY 428 WSRNLSVDWKRTPPCGRRGCGSVLTVTHTSTSSQSQVAHAHAWCLSLAKLPSPADSLT 487
DB 473 WSRWTLALDFKRAKSGSSSY-SYGPVMSHTSVTVNVPRAGLGLSPRLIPALAAATTA 531
QY 488 ATSLVMSGVYQSRATSHL-----STRSKED-----SGRQRDILMEXPSRPMES 535
DB 532 TTNGHPPIPGHT--KPGAPTLPATPPATAAPKDDOGLNGSCSLDEASAPERPPALQOE 589
QY 536 NPDT 539
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DB 590 EWET 593

RESULT 6
QY1WV4 PRELIMINARY; PRT; 591 AA.
ID Q91WV4 AC Q91WV4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Parathyroid hormone receptor.
GN PTHR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013446; AAH13446.1; -.
DR MGD; MGI:97801; Pthr.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7cm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 591 AA; 66361 MW; 6E29CF63E5BAFEED CRC64;

Query Match 45.6%; Score 1324.5; DB 11; Length 591;
Best Local Similarity 50.5%; Pred. No. 1.5e-113;
Matches 258; Conservative 75; Mismatches 117; Indels 61; Gaps 7;

QY 22 ARAQLSDGTITIEQIVLVKAKVQCE-----INITAIQVQEGN----- 62
DB 22 AVALVDADDVFTKERQIFLLHRAQAQCKLLEKLVLTAAANIMESDKGWTPASTSGKPKKE 81
QY 63 -----CFPEWDLICWPR-----GYACRVAVTFFLYFLA----- 141
DB 82 KAPGKFPESKENKDVPTGSRGRGRCLEPWHILCWPLGAPGVAVVPCPDYIDFNH 141
QY 97 GYAFHCPNPGTWDFMHSLNKTNWYSDCLRFLOPDISIGKQFCERLYVWYTVGYSIS 156
DB 142 GHAYRCDRNGSWELVPCHNRTWANYSECVKELTNETR--EREVFDRLGMIYTVGYS 199
QY 157 GSLAVAILIIGYFRRLHCTRNYYHMLFVSPMLRATSIYVQDVVVAHIGVKELES!--- 213
DB 200 ASLTAVAILAYFRRLHCTRNYYHMLFVSPMLRAASIFVKDAVLYSGFTLDEARLTEE 259
QY 214 ----IMQDDPQNSIEATSDKSOYIGCKIAVWVFYFLATNYTWILVEGLYLNHLIFVAF 269
DB 260 ELHIITAIQVPPPPAAAAG-----YACRVAVTFFLYFLATNYTWILVEGLYLNHLIF 314
QY 270 FSDTKYLWGLFILGWGFPAAFVAWAVARATLADARWEKAGDIKIYQAPILAAIGLN 329
DB 315 FSEKYLWGLTIFGNGLPVAVVAVVAVRATLANTGCDLSSGHKKWIIQVPIASVVLN 374
QY 330 FILPLNTVRVLAETKIETNAVGHDTKQYRKLAKSTLVLVIFVGHVIVFVCLPHS--FTG 388
DB 375 FILFINIIRVLAETKIETNAVGHDTKQYRKLAKSTLVLVIFVGHVIVFVCLPHS--FTG 434
QY 389 LQWEIRMHCELFNSFGGFVSIYCYCNAGEVQAEVKKMWSRNLSDWKETPPCGSRRC 448
DB 435 TLWQIQMHYEMLFNSFGGFVSIYCYCNAGEVQAEVKKMWSRNLSDWKETPPCGSRRC 494
QY 449 GSVLTVTHTSTSSQSQVAHAHAWCLSLAKLP 479

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Db 572 WILVEGLYLSLIPMAFFSEKKYLMGFTVFGWGLPAVFAVAVVSVRATLANTGVQPPDA- 630
 QY 313 DIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQY- 358
 Db 631 -----APSLFQ--LNFILFINVRVLATKIWETNAGRCDDTQQVYRGSGGLATYLPWP 681
 QY 359 KKLAKSTLVLMVFGVHYIVFVCLPHS-FTGLGWEIRMHCELFNSF- 404
 Db 682 KKLKSTLVLMPLFGVHYIVFMATPYTEVSTLMQVMHVELFNSFQVRSAGGLAEGG 741
 QY 405 -----QGFVSIICYNGEVOAEVKQWGSWNIIVDWKRTPPCGSRG- 449
 Db 742 RSGGGRPDRHPSQGFVAIYFCNCEVQAEIKKSWRTLALDFKGRKARSGSSYSY 801
 QY 450 SVLTFTVHTSSQSQVAAAHAWCLSLAKLPRSPADSLTATSL-YLAMSGVTOQSKT-ASHT 507
 Db 802 GPMVSHSTVTVNGRVLG-----LPLSPRLPTATNGHPQIPGHAKGTGPALET 852
 QY 508 LSTRS-----NKEDSGQRDDILMEKPSRPMESNPDTEG 541
 Db 853 LETTPPAAAPKDDGFLNGSCGLDEASGPERPALLQBEWETVISGDHLEG 905

RESULT 9

Q9R1D4
 ID Q9R1D4 PRELIMINARY; PRT; 169 AA.
 AC Q9R1D4
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Parathyroid hormone type-2 receptor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99367425; PubMed=10438471;
 RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
 RT "A G protein-coupled receptor from zebrafish is activated by human
 RT parathyroid hormone and not by human or teleost parathyroid hormone-
 RT related peptide. Implications for the evolutionary conservation of
 RT calcium-regulating peptide hormones.";
 RL J. Biol. Chem. 274:23035-23042 (1999).
 DR EMBL; AF132083; AAD51909.1; -
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 FT NON TER 1 1
 FT TER 169 169
 SQ SEQUENCE 169 AA; 19674 MW; 748CC8231F1C69EA CRC64;

Query Match 29.5%; Score 858.5; DB 11; Length 169;
 Best Local Similarity 92.9%; Pred. No. 3.5e-71;
 Matches 158; Conservative 4; Mismatches 7; Indels 1; Gaps 1;
 QY 250 NYWILVEGLYLNLIIFVAFPSDTKYLWGFTILGWGFPFAAFVAAVARATLADARCNEL 309
 Db 1 NYWILVEGLYLNLIIFVAFPSDTKYLWGFTILGWGFPFAAFVAAVARATLADARCNEL 60
 QY 310 SAGDIKWTYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYKRLAKSTLVLV 369
 Db 61 SAGD--RWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDMRKQYKRLAKSTLVLV 119
 QY 370 LVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFQGFVSIICYNGE 419
 Db 120 LVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFQGFVSIICYNGE 169

RESULT 10

Q9YHC6
 ID Q9YHC6 PRELIMINARY; PRT; 444 AA.
 AC Q9YHC6
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Vasoactive intestinal peptide/pituitary adenylate cyclase activating
 DE polypeptide receptor.
 OS Rana ridibunda (laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Anura; Neobatrachia; Ranioidea; Rana.
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=99165178; PubMed=10067855;
 RA Alexandre D., Anouar Y., Jegou S., Fournier A., Vaudry H.;
 RT "A cloned frog vasoactive intestinal polypeptide/pituitary adenylate
 RT cyclase-activating polypeptide receptor exhibits pharmacological and
 RT tissue distribution characteristics of both VPAC1 and VPAC2 receptors
 RT in mammals.";
 RL Endocrinology 140:1285-1293 (1999).
 DR EMBL; AF100644; AAD03602.1; -
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 SQ SEQUENCE 444 AA; 50955 MW; 863B25E729314C4C CRC64;

Query Match 28.0%; Score 814; DB 13; Length 444;
 Best Local Similarity 36.8%; Pred. No. 1.5e-66;
 Matches 168; Conservative 73; Mismatches 133; Indels 82; Gaps 12;
 QY 41 VLKAKVQCELNITATLQOE- 89
 Db 17 ILCPVEECSIMVQIELKHEECVHEDYENDTAVCKRTWDNITCWPASIGEVVVLQCEGY 76
 QY 90 IYDFNH---KGAFPHCNPNGTWDFMHSLNKTNWYNSDCLRFLOPDISIGKQE-FCBRLY 145
 Db 77 FSMFTTGTWNGVGNKCTSEG-WSEMYV-----ATYAAACGFTNDTPTQOQTVFFGAIK 130
 QY 146 VMYTVGYSISFGSLAVAILIIGYFRLHCTRNHYHMLFVSEFMLRATSIYKDRV- 201
 Db 131 TGYTIGHSLSLSLTAAMIIICIFKHLCTRNHYHMLFVSEFMLRATSIYKDRV- 190
 QY 202 ---HAHIGVKELESIMQDDPQNSIEATSDKSYIGCKIAVVMFIYPLATNYWILVEG 258
 Db 191 ESDHCHVG-----SVGCKAAMVFFQYICIMANFVLLVEG 224
 QY 259 LYLHNLIFVAFPSDTKYLWGFTILGWGFPFAAFVAAVARATLADARCNELAKSTLVLV 318
 Db 225 LYLHNLIVISFFSEKKYFWWYILIGWGFVITANSLARYFEDTGCWDTIESHLMWII 284
 QY 319 QAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYKRLAKSTLVLVFGVHYIV 378
 Db 285 KTPILVSLVNVNFIICIRILVQKLHSPD-VGRNENSOYTRLAKSTLVLLPLFGVHYIM 343
 QY 379 FVCLPHSFTGLGWEIRMHCELFNSFQGFVSIICYNGEVOAEVKQWGSWNIIV 434
 Db 344 FAFFPDNFK---VEVKLVFELILGSFQGVVAVLYCFNLNGEVQAEKLRKWRNLERPMW 400
 QY 435 VDMK-RTPCGS-----RRCGS 450
 Db 401 KDMKYHPSLNGSNGTNFTQISMLTKCSPKTRCRSS 436

RESULT 11

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Q8BUM8
ID Q8BUM8 PRELIMINARY; PRT; 237 AA.
AC Q8BUM8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Parathyroid hormone receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
KP STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK083278; BAC38840.1; -.
FT NON_TER 1
SQ SEQUENCE 237 AA; 26863 MW; PA35AC19CIF5257 CRC64;

Query Match 27.8%; Score 803.5; DB 11; Length 237;
Best Local Similarity 70.0%; Pred. No. 6.4e-66;
Matches 163; Conservative 15; Mismatches 48; Indels 7; Gaps 3;

QY 312 GDKIWIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDRKQYRKLAKSTLVLV 371
DB 1 GD-RWYIQAPILAAIGLNFILNTVRLATKIWETNAVGHDRKQYRKLAKSTLVLV 59
QY 372 FGVIYIVFVCLPHSFTGLGWIRMHCELFNSFGFFVSIYCYNGEVAQVKKQWRW 431
DB 60 FGVIYIVFVCLPHSFTGLGWIRMHCELFNSFGFFVSIYCYNGEVAQVKKQWRW 119
QY 432 NLSVDWKRPCCSRRCGSLVTTVTHSTSSQSOVAHAHAWCLSLAKLPRSPA---DSLTA 488
DB 120 NLSVDWKRPCCSRRCGSLVTTVTHSTSSQSOVAHAHAWCLSLAKLPRSPA---DSLTA 179
QY 489 TSLYLAMSGVQRTASHTLSTRNKEDSGRQDDILMBKPRPMSNPDTGEG 541
DB 180 LPCYVWSSSQDCQTHSPPEET---KEGHRQGDSDPVMSESRPVAFTLDTEG 229

RESULT 12
Q8AXV3
ID Q8AXV3 PRELIMINARY; PRT; 419 AA.
AC Q8AXV3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vasoactive intestinal peptide receptor 1 A.
GN VIPRIA.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
SEQUENCE FROM N.A.
RA Cardoso J.C.R., Power D.M., Canario A.V.M., Elgar G., Clark M.S.;
RT "Isolation and characterisation of the VIPR/PACAP receptor gene family
RT in Fugu rubripes."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296144; CAC82588.1; -.
KW Receptor.
SQ SEQUENCE 419 AA; 47607 MW; F21C006AA4E1B698 CRC64;

Query Match 27.3%; Score 794; DB 13; Length 419;
Best Local Similarity 36.9%; Pred. No. 9.8e-65;
Matches 175; Conservative 82; Mismatches 127; Indels 90; Gaps 15;

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QY 47 QCE---LNTAQLQEGEGNCFPEWDGLICWPRGTGKISAVPCPPYIDFN--HKGVAFR 101
DB 14 RCENSVENVTA-----GCGQWMDIIACWPSAGVGEVVTITCTVYFSPDQHKGNLSK 66
QY 102 HCPNPGTWDMHSLNKWTWANYSCDLRFLQPDISG-----KQFCERLYVMYTVG 151
DB 67 TCTADG-WTEMHPL-----DIAVNCGYNVNGTSDGDNFLMQVKIGYTVG 109
QY 152 YSISFGSLAVAILIIGYFRHLHCTRNVIHMHLPVSMFLRATSIKRVVVAHIGVKELE 211
DB 110 YSVLSLITAIIVLICTFRKLHCTRNVIHMHLPVSMFLRATSIKRVVVAHIGVKELE 156
QY 212 SLIMQDPQNSIEATSDVKQYIGCKIAVVMFYFLATNYYIWLVEGLYHNLIFVAFPS 271
DB 167 DC-----SSGTIGCKVIVFFQYCIAMSPFLLVEGLYHALLAVSFFS 210
QY 272 DTKYLNGFILLGWFPAFVAAMAVARATLADARWE--LSAGDIK-WIYQAPILAAIGLN 329
DB 211 ERKYFSAYILIGWGPTVFIAAWSVAKAYTYDGCWMDIIESNDMSMWIIKTPIIASILIN 270
QY 330 FILELNTVRVLATKIWETNAVGHDRKQYRKLAKSTLVLVFVGVHYIVFVCLPHSFTGL 389
DB 271 FILFICIIIRILROKI-NCPDIGRNESQYSELAKSTLLIPLFGINFIYFAFIPEQ---V 326
QY 390 GWEIRMHCELFNSFGFFVSIYCYNGEVAQVKKQWRWML-----SVDWKRTPPCGS 445
DB 327 KTELRLVFDLTLGSGFGVAVLYCFLNGEVOGEIKRKRWRHLQRYMSSDAKYQP---383
QY 446 RCRCGSLVTTVTHSTSSQSOVAHAHAWCLSLAKLPR-SPADSLTATSLYLAMSGV 498
DB 384 -----SIGSSNNFTQISMLPRCSPKTRRASSCHDDLSSI 419

RESULT 13
Q9JI40
ID Q9JI40 PRELIMINARY; PRT; 459 AA.
AC Q9JI40;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vasoactive intestinal peptide receptor type 1 (Vasoactive intestinal
DE peptide receptor 1).
GN VIPRI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Karacay B., O'Dorisio M.S., Kasow K., Krahe R.;
RT "Cloning and Fine Mapping of the Vasoactive Intestinal Peptide
RT Receptor 1 (VPAC1): A Comparative Analysis of Human, Rat and Murine
RT genes."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AF266282; AAF77053.1; -.
DR EMBL; AK052465; BAC35004.1; -.
DR MGD; MGI:109272; Vipri.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; normn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.

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Db 258 LHCTRYIHMLFVSFILRALSFIKDAV-----LFSSDD-----VTYCD-A 298
QY 232 QYIGCKIAVVMFYFLATNYWYLLVEGLYHNLIFVAFESDTKYLWGRFLLIGWGFPAAFV 291
Db 299 HRAGCKLIWVLFQYCIIMANYWMLVEGLYHNLIFVAFESDTKYLWGRFLLIGWGFPAAFV 358
QY 292 AAWAVARATLADARCWELSA-GDIKWIYQAPILAAIGLNFILNTRVRLATKIWETNAV 350
Db 359 ALWAIARHFLEDVGCWDINANASIWIIIRGPVILSILINILFINILRILMEKLTQETR 418
QY 351 GHDTKQYKRLAKSTLVVLVGVVHYIVFVCLPHSFTGLGWEIRHCELFNSFQGFVVS 410
Db 419 GNEV-SHYKRLARSTLLIPLFGIHYIVFAFSPED----AMEIQLEFFELALGSFQGLVVA 473
QY 411 IYCYCNGEVOAEVKQWGRWNLSDVKRTPPCGSRRCGSLTTVTHSTSSQ 462
Db 474 VLYCFUNGVEVQKQWQWHL-----REFPLHPVAFSFSNSTKASHLEQSQ 520

Search completed: November 21, 2003, 22:27:24
Job time : 41 secs